

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 3, 2005, 08:53:28 ; Search time 7.09576 Seconds

(without alignments)
1545.812 Million cell updates/sec

Title: US-10-791-619-8

Perfect score: 596

Sequence: 1 DIQLTQSPSSLSASVGDVRT.....SHEDPYTFGQGTKEIKRTV 114

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	498	83.6	127	2 S40367	Ig kappa chain V-J
2	487	81.7	123	2 S40331	Ig kappa chain - h
3	486	81.5	108	2 B49047	Ig kappa chain V r
4	475	79.7	109	2 S31998	Ig kappa chain - h
5	471	79.0	108	2 S44122	Ig kappa chain V r
6	470	78.9	120	2 S46370	Ig kappa chain V-J
7	469	78.7	108	2 S47182	Ig kappa chain - h
8	468	78.5	109	2 S31981	Ig kappa chain - h
9	465.5	78.1	125	2 S40315	Ig kappa chain - h
10	464	77.9	108	1 KIHURU	Ig kappa chain V-I
11	462	77.5	108	2 S19674	Ig kappa chain V r
12	462	77.5	122	2 S40370	Ig kappa chain - h
13	462	77.5	132	2 S40334	Ig kappa chain - h
14	461	77.3	129	2 S52793	Ig kappa chain V r
15	459	77.0	129	2 S52792	Ig kappa chain V r
16	458	76.8	107	2 S36264	Ig kappa chain V
17	457	76.7	117	2 S46371	Ig kappa chain V-J
18	457	76.7	122	2 S40314	Ig kappa chain - h
19	457	76.7	125	2 S40333	Ig kappa chain V-J
20	457	76.7	129	2 S40317	Ig kappa chain - h
21	456.5	76.6	124	2 S40336	Ig kappa chain V-J
22	456	76.5	108	1 KIHUDE	Ig kappa chain V-I
23	456	76.5	129	2 S40369	Ig kappa chain - h
24	456	76.5	131	2 S40352	Ig kappa chain V-J
25	455	76.3	109	2 S31979	Ig kappa chain - h
26	455	76.3	109	2 S31978	Ig kappa chain - h
27	454	76.2	125	2 S40350	Ig kappa chain - h
28	453	76.0	129	1 KIHUKV	Ig kappa chain pre
29	452	75.8	126	2 S40335	Ig kappa chain V-J

30	451	75.7	109	2 S31980	Ig kappa chain - h
31	451	75.7	125	2 S40349	Ig kappa chain V-J
32	450	75.5	108	1 KIHUOU	Ig kappa chain V-I
33	450	75.5	130	2 S40368	Ig kappa chain - h
34	449.5	75.4	107	2 S36275	Ig lambda chain V
35	449	75.3	107	2 JLO139	Ig kappa chain V r
36	448	75.2	109	2 S32001	Ig kappa chain - h
37	448	75.2	109	2 S31983	Ig kappa chain - h
38	448	75.2	128	2 S46372	Ig light chain var
39	447	75.0	108	2 S31977	Ig kappa chain - h
40	447	75.0	117	2 S46376	Ig kappa chain V-J
41	447	75.0	125	2 S40316	Ig kappa chain - h
42	445	74.7	108	1 KIHUUA	Ig kappa chain V-I
43	445	74.7	108	1 KIHURN	Ig kappa chain V-I
44	443	74.3	108	1 KIHULY	Ig kappa chain V-I
45	443	74.3	129	2 S52789	Ig kappa chain V r

ALIGNMENTS

RESULT 1

S40367

Ig kappa chain V-J-C region - human

C:Species: Homo sapiens (man)

C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C:Accession: S40367

Eur. J. Immunol. 23, 3248-3271, 1993

R.Klein, R.; Jaenichen, R.; Zachau, H.G.

A:Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8258341

A:Accession: S40367

A>Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-127 <KLE>

A:Cross-references: EMBL:X72477

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:33-107/Domain: immunoglobulin homology <IMM>

Query Match 83.6%; Score 498; DB 2; Length 127;
Best Local Similarity 85.1%; Pred. No. 1.3e-36;
Matches 97; Conservative 5; Mismatches 5; Indels 4; Gaps 1;

QY 1 DIQLTQSPSSLSASVGDVRTTTCRASKPVDEGDSYLNWYQOKPKAPKLLIYAASYLE 60

DB 18 DIQMTQSPSSLSASVGDVRTTTCRASQSI---SNLWYQOKPKAPKLLIYAASLSQS 73

QY 61 GVPGRFSGSGGTDTLTITSSLOPEDFATYYCQOSHEDPYTFGQGTKEIKRTV 114

DB 74 GVPGRFSGSGGTDTLTITSSLOPEDFATYYCQOSHEDPYTFGQGTKEIKRTV 127

RESULT 2

S40331

Ig kappa chain - human

C:Species: Homo sapiens (man)

C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C:Accession: S40331

Eur. J. Immunol. 23, 3248-3271, 1993

A:Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891; PMID:8258341

A:Accession: S40331

A>Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-123 <KLE>

A:Cross-references: EMBL:X72441; NID:G441350; PIDN:CAA51109.1; PID:G441351

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:32-106/Domain: immunoglobulin homology <IMM>

Query Match 81.7%; Score 487; DB 2; Length 123;

Best Local Similarity 86.5%; Pred. No. 1.2e-35; Mismatches 5; Indels 4; Gaps 1;
Matches 96; Conservative 5; Mismatches 6; Indels 4; Gaps 1;
QY 1 DIQLTQSPSSLSASVGRVVTITCRASPVDEGDSYLNWYQKPGKAPKLLIYAASLYS 60
Db 17 DIQLTQSPSSLSASVGRVVTITCRASQSI----SSYLNWYQKPGKAPKLLIYAASLSQS 72
QY 61 GVPSRFGSGSGTDFTLTISLQPEDFATYYCQOSHEDPYTFGGTKVEIK 111
Db 73 GVPSRFGSGSGTDFTLTISLQPEDFATYYCQOSYSTPTFTGGTKVEIK 123
RESULT 3
B49047
Ig kappa chain V region (monoclonal striational autoantibody StrAB SA-1A) - human (fragm
C;Species: Homo sapiens (man)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: B49047
R;Victor, K.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.
Eur. J. Immunol. 22, 2231-2236, 1992
A;Title: Human monoclonal striational autoantibodies isolated from thymic B lymphocytes
A;Reference number: A49047; MUID:92387224; PMID:1516616
A;Accession: B49047
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-108 <VIC>
A;Cross-references: UNIPROT:Q96SA9; UNIPROT:Q9UL77
A;Experimental source: thymic B lymphocytes
A;Note: sequence extracted from NCBI backbone (NCBIN:113208, NCBIPI:113209)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>
Query Match 81.5%; Score 486; DB 2; Length 108;
Best Local Similarity 85.7%; Pred. No. 1.2e-35; Indels 4; Gaps 1;
Matches 96; Conservative 5; Mismatches 7; Indels 4; Gaps 1;
QY 1 DIQLTQSPSSLSASVGRVVTITCRASPVDEGDSYLNWYQKPGKAPKLLIYAASLYS 60
Db 1 DIQLTQSPSSLSASVGRVVTITCRASQSI----SSYLNWYQKPGKAPKLLIYAASLSQS 56
QY 61 GVPSRFGSGSGTDFTLTISLQPEDFATYYCQOSHEDPYTFGGTKVEIK 112
Db 57 GVPSRFGSGSGTDFTLTISLQPEDFATYYCQOSYSTPTFTGGTKVEIK 108
RESULT 4
S31998
Ig kappa chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C;Accession: S31998
R;Portolano, S.; Chazembalk, G.D.; Hutchison, S.J.; McLachlan, S.M.; Rapoport, B.
submitted to the EMBL Data Library, June 1992
A;Description: Lack of promiscuity in autoantigen-specific H and L chain combinations as
A;Reference number: S31977
A;Accession: S31998
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-109 <POR>
A;Cross-references: EMBL:Z15081; NID:g38501; PIDN:CAA78790.1; PID:g38502
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>
Query Match 79.7%; Score 475; DB 2; Length 109;
Best Local Similarity 80.5%; Pred. No. 1.1e-34; Indels 4; Gaps 1;
Matches 91; Conservative 12; Mismatches 6; Indels 4; Gaps 1;
QY 1 DIQLTQSPSSLSASVGRVVTITCRASPVDEGDSYLNWYQKPGKAPKLLIYAASLYS 60
Db 1 ELVNTQSPSSLSASVGRVVTITCRASQSI----SAYLNWYQKPGKAPKLLIYAASLSQS 56
QY 61 GVPSRFGSGSGTDFTLTISLQPEDFATYYCQOSHEDPYTFGGTKVEIK 113

Db 57 GVPSRFGSGSGTDFTLTISLQPEDFATYYCQOSYDTPWTFGHGKVEIKRT 109
RESULT 5
S44122
Ig kappa chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C;Accession: S44122
R;Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
submitted to the EMBL Data Library, March 1994
A;Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable re
A;Reference number: S44105
A;Accession: S44122
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-108 <HAW>
A;Cross-references: EMBL:Z31390; NID:g472976; PIDN:CAA83265.1; PID:g940533
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>
Query Match 79.0%; Score 471; DB 2; Length 108;
Best Local Similarity 83.0%; Pred. No. 2.5e-34; Indels 4; Gaps 1;
Matches 93; Conservative 7; Mismatches 8; Indels 4; Gaps 1;
QY 1 DIQLTQSPSSLSASVGRVVTITCRASPVDEGDSYLNWYQKPGKAPKLLIYAASLYS 60
Db 1 DIQLTQSPSSLSASVGRVVTITCRASQSI----SSYLNWYQKPGKAPKLLIYAASLSQS 56
QY 61 GVPSRFGSGSGTDFTLTISLQPEDFATYYCQOSHEDPYTFGGTKVEIK 112
Db 57 GVPSRFGSGSGTDFTLTISLQPEDFATYYCQOSYSTPTWTFGGTKVEIK 108
RESULT 6
S46370
Ig kappa chain V-J region (T23-9) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 27-Jan-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
C;Accession: S46370; S38644
R;Bensimon, C.; Chaatagner, P.; Zouali, M.
EMBO J. 13, 2951-2962, 1994
A;Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene re
A;Reference number: S46369; MUID:94313975; PMID:8039491
A;Accession: S46370
A;Molecule type: mRNA
A;Residues: 1-120 <BEN>
A;Cross-references: EMBL:Z27171; NID:g415957; PIDN:CAA81695.1; PID:g415958
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;26-100/Domain: immunoglobulin homology <IMM>
Query Match 78.9%; Score 470; DB 2; Length 120;
Best Local Similarity 81.6%; Pred. No. 3.4e-34; Indels 6; Gaps 2;
Matches 93; Conservative 8; Mismatches 7; Indels 6; Gaps 2;
QY 1 DIQLTQSPSSLSASVGRVVTITCRASPVDEGDSYLNWYQKPGKAPKLLIYAASLYS 60
Db 11 DIQLTQSPSSLSASVGRVVTITCRASQSI----SSFLNWYQKPGKAPQLLIYAVSRLQS 66
QY 61 GVPSRFGSGSGTDFTLTISLQPEDFATYYCQOSHEDP--YTFGQGTKEIKR 112
Db 67 GVPSRFGSGSGTDFTLTISLQPEDFATYYCQOSFNPPEYTFGQGTKEIKR 120
RESULT 7
S47182
Ig kappa chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S47182

A:Molecule type: mRNA
A:Residues: 1-108 <RMB>
C:Cross-references: EMBL:X61642; NID:g937860; PIDN:CAA43823.1; PID:g1335386
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 77.5%; Score 462; DB 2; Length 108;
Best Local Similarity 81.2%; Pred. No. 1.5e-33;
Matches 91; Conservative 9; Mismatches 8; Indels 4; Gaps 1;

QY 1 DIQLTSPSSLSASVGRDVITTCRASPVDEGDSYLNNWYQOKPGKAPKLLIYAASVLES 60
Db 1 EIVLTQSPSSLSASVGRDVITTCRASQSI---SNLYNWYQOKPGKAPKLLIYAASLTQS 56
QY 61 GVPSRFSGSGGTDTFTLTISLQPEDPATYYCQOSHEDPVTFFGGTKVEIKR 112
Db 57 GVPSRFSGSGGTDTFTLTINSLQPEDPATYYCQQTNSFPPLTFGGGTKLEIKR 108

RESULT 12
S40370
Ig kappa chain - human
C:Species: Homo sapiens (man)
C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40370
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40370
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-122 <KLE>
A:Cross-references: EMBL:X72480; NID:g441428; PIDN:CAAS1148.1; PID:g441429
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:30-104/Domain: immunoglobulin homology <IMM>

Query Match 77.5%; Score 462; DB 2; Length 122;
Best Local Similarity 82.1%; Pred. No. 1.7e-33;
Matches 92; Conservative 7; Mismatches 9; Indels 4; Gaps 1;

QY 1 DIQLTSPSSLSASVGRDVITTCRASPVDEGDSYLNNWYQOKPGKAPKLLIYAASVLES 60
Db 15 DIQLTQSPSSLSASVGRDVITTCRASQSI---STFLHWQQNLGXAPKLLIYAASNLS 70
QY 61 GVPSRFSGSGGTDTFTLTISLQPEDPATYYCQOSHEDPVTFFGGTKVEIKR 112
Db 71 GVPSRFSGSGGTDTFTLTISGLQPEDPATYYCQOSYTTPRTFGGTKVEIKR 122

RESULT 13
S40334
Ig kappa chain - human
C:Species: Homo sapiens (man)
C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40334
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40334
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-132 <KLE>
A:Cross-references: EMBL:X72444
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:37-111/Domain: immunoglobulin homology <IMM>

Query Match 77.5%; Score 462; DB 2; Length 132;
Best Local Similarity 79.8%; Pred. No. 1.9e-33;

Search completed: June 3, 2005, 09:17:50
Job time : 8.09576 secs

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OM protein - protein search, using sw model

Run on: June 3, 2005, 08:31:37 ; Search time 32.7497 Seconds
(without alignments)
1782.523 Million cell updates/sec

Title: US-10-791-619-8

Perfect score: 596

Sequence: 1 DIQLTQSPSSLASVGDVDT.....SHEDPYTFGQTKVIEKRTV 114

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03:*

1: uniprot_prot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	481	80.7	236	2	Q6GMX8	Q6gmX8 homo sapien
2	480	80.5	108	2	Q9UL77	Q9ul77 homo sapien
3	470	78.9	236	2	Q6GMW1	Q6gmW1 homo sapien
4	468.5	78.6	107	2	Q96SA9	Q96sa9 homo sapien
5	466	78.2	236	2	Q6GMX0	Q6gmX0 homo sapien
6	465	78.0	236	2	Q6PIH7	Q6pih7 homo sapien
7	464	77.9	108	1	KV1H_HUMAN	P01600 homo sapien
8	456	76.5	108	1	KV1E_HUMAN	P01597 homo sapien
9	453	76.0	129	1	KV1W_HUMAN	P04431 homo sapien
10	450	75.5	108	1	KV1N_HUMAN	P01606 homo sapien
11	446	74.8	236	2	Q723Y4	Q723y4 homo sapien
12	445	74.7	108	1	KV1B_HUMAN	P01594 homo sapien
13	445	74.7	108	1	KV1V_HUMAN	P04430 homo sapien
14	443.5	74.4	107	2	Q9UL81	Q9ul81 homo sapien
15	443	74.3	108	1	KV1M_HUMAN	P01605 homo sapien
16	442	74.2	108	2	Q9UL70	Q9ul70 homo sapien
17	442	74.2	234	2	Q72473	Q72473 homo sapien
18	441	74.0	111	1	KV3M_MOUSE	P01665 mus musculus
19	440	73.8	108	1	KV1K_HUMAN	P01603 homo sapien
20	440	73.8	108	1	KV1O_HUMAN	P01607 homo sapien
21	438	73.5	108	1	KV1S_HUMAN	P01611 homo sapien
22	437	73.3	236	2	Q6GMX9	Q6gmX9 homo sapien
23	436	73.2	108	1	KV1P_HUMAN	P01598 homo sapien
24	436	73.2	108	1	KV1J_HUMAN	P01599 homo sapien
25	436	73.2	108	1	KV1Y_HUMAN	P01602 homo sapien
26	436	73.2	111	1	KV3O_MOUSE	P01667 mus musculus
27	434	72.8	108	1	KV1P_HUMAN	P01608 homo sapien
28	434	72.8	111	1	KV3N_MOUSE	P01666 mus musculus
29	434	72.8	236	2	Q6PII5	Q6pii5 homo sapien
30	433	72.7	108	1	KV1R_HUMAN	P01610 homo sapien
31	433	72.7	111	1	KV3L_MOUSE	P01664 mus musculus

32	433	72.7	111	1	KV3Q_MOUSE	P01669 mus musculus
33	431	72.3	108	2	Q9UL79	Q9ul79 homo sapien
34	429	72.0	108	1	KV1L_HUMAN	P01604 homo sapien
35	429	72.0	236	2	Q6PIH4	Q6pih4 homo sapien
36	427	71.6	116	2	Q96PF6	Q96pf6 homo sapien
37	427	71.6	244	2	Q65ZC8	Q65zc8 homo sapien
38	425	71.3	108	1	KV1A_HUMAN	P01593 homo sapien
39	424.5	71.2	107	1	KV1D_HUMAN	P01596 homo sapien
40	423.5	71.1	109	1	KV1T_HUMAN	P01612 homo sapien
41	423	71.0	111	1	KV3H_MOUSE	P01660 mus musculus
42	423	71.0	240	2	Q65ZC9	Q65zc9 homo sapien
43	422	70.8	108	1	KV1Q_HUMAN	P01609 homo sapien
44	422	70.8	111	2	Q81IU6	Q81iu6 mus musculus
45	421	70.6	108	1	KV1C_HUMAN	P01595 homo sapien

ALIGNMENTS

RESULT 1

ID	Q6GMX8	PRELIMINARY;	PRT;	236 AA.
AC	Q6GMX8;			
DT	05-JUL-2004 (Tremblrel. 27, Created)			
DT	05-JUL-2004 (Tremblrel. 27, Last sequence update)			
DT	05-JUL-2004 (Tremblrel. 27, Last annotation update)			
DE	Hypothetical protein.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini, Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
SEQUENCE FROM N.A.				
RP	TISSUE=Primary B-Cells;			
RC	MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Hopkins R.F., Zeeberg B., Buotow K.H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalón D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.,			
RA	Krzywinski M.I., Skalska U., Smalius D.E., Schnerch A., Schein J.E.,			
RT	Jones S.J., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RL	and mouse cDNA sequences."			
Proc. Natl. Acad. Sci. U.S.A.	99:16899-16903(2002).			
[2]				
SEQUENCE FROM N.A.				
RP	TISSUE=Primary B-Cells;			
RC	Submitted (JUN-2004) to the EMBL/GenBank/DBSJ databases.			
RA	Strausberg R.;			
DR	EMBL; BC073764; AAH73764.1; -.			
DR	InterPro; IPR003599; IG.			
DR	InterPro; IPR007110; IG-like.			
DR	InterPro; IPR003597; IG cl.			
DR	InterPro; IPR003006; IG_MHC.			
DR	InterPro; IPR003596; IG_v.			
DR	Pfam; PF07654; Cl-set; 1.			
DR	Pfam; PF00047; IG; 2.			
DR	SMART; SM00409; IG; 2.			
DR	SMART; SM00407; IGcl; 1.			
DR	SMART; SM00406; IGv; 1.			
DR	PROSITE; PS50835; IG_LIKE; 2.			
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_1.			

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KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25707 MW; 4FC8E14B6559EFC9 CRC64;

Query Match      80.7%; Score 481; DB 2; Length 236;
Best Local Similarity 82.5%; Pred. No. 6.3e-40;
Matches 94; Conservative 9; Mismatches 7; Indels 4; Gaps 1;

Qy 1 DIQQTQSPSSLSASVGRVITTCRASKPVDCGDSYLNWYQKPGKAPKLLIYAASYLE 60
Db 23 DIQMTQSPSSVSASVGRVITTCRASQGI---SSWLAWYQKPGKAPKLLIYAASLSQ 78

Qy 61 GVPFRFSGSGGTDFTLTITSLQPEDPATYCCQSHEDPYTFGQGTKEIKRTV 114
Db 79 GVPFRFSGSGGTDFTLTITSLQPEDPATYCCQSHSPFTFGRTKVDIKRTV 132

RESULT 2
Q9UL77 PRELIMINARY; PRT; 108 AA.
AC Q9UL77;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RZ MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clim.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL; AF035037; AA056273.1; -.
DR PIR; B49047; B49047.
DR PIR; S34083; S34083.
DR HSP; P01607; 1BWW.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 108
FT SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match      80.5%; Score 480; DB 2; Length 108;
Best Local Similarity 83.9%; Pred. No. 3.3e-40;
Matches 94; Conservative 7; Mismatches 7; Indels 4; Gaps 1;

Qy 1 DIQQTQSPSSLSASVGRVITTCRASKPVDCGDSYLNWYQKPGKAPKLLIYAASYLE 60
Db 1 DIQMTQSPSSLSASVGRVITTCRASQGI---SSYLNWYQKPGKAPKLLIYAASLSQ 56

Qy 61 GVPFRFSGSGGTDFTLTITSLQPEDPATYCCQSHEDPYTFGQGTKEIKR 112
Db 57 GVPFRFSGSGGTDFTLTITSLQPEDPATYCCQSHSYSTSWTFGRTKVEIKR 108

RESULT 3
Q6GMW1 PRELIMINARY; PRT; 236 AA.
AC Q6GMW1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RZ MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Moore H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RZ MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clim.1998.4531;
RA Strausberg R.;
RT Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073791; AAH73791.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 1.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25751 MW; 5BFE6A087AFAC437 CRC64;

Query Match      78.9%; Score 470; DB 2; Length 236;
Best Local Similarity 82.3%; Pred. No. 7.9e-39;
Matches 93; Conservative 7; Mismatches 9; Indels 4; Gaps 1;

Qy 2 IQLTQSPSSLSASVGRVITTCRASKPVDCGDSYLNWYQKPGKAPKLLIYAASYLESG 61
Db 24 IQMTQSPSSLSASVGRVITTCRASQGI---LCWYQKPGKAPKLLIYAASLSQSG 79

Qy 62 VPSRFSGSGGTDFTLTITSLQPEDPATYCCQSHEDPYTFGQGTKEIKRTV 114
Db 80 VPSRFSGSGGTDFTLTITSLQPEDPATYCCQSHEDPYTFGQGTKEIKRTV 132

RESULT 4
Q96SA9 PRELIMINARY; PRT; 107 AA.
AC Q96SA9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Anti-streptococcal/anti-myosin immunoglobulin kappa light chain
DE variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
```


RP	SEQUENCE FROM N.A.
RX	MEDLINE=98375893; PubMed=97112075;
RA	Adderson E.E., Shikhman A.R., Ward K.E., Cunningham M.W.;
RT	"Molecular analysis of polyclonal antibodies from
RT	rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
RL	antibody v region genes.";
JL	J. Immunol. 161:2020-2031(1998).
DR	EMBL; U96396; AAB68785.1; -.
DR	PIR; B49047; B49047.
DR	PIR; PH0867; PH0867.
DR	PIR; S16840; S16840.
DR	PIR; S31977; S31977.
DR	PIR; S34083; S34083.
DR	PIR; S34086; S34086.
DR	HSP; P01607; IEMW.
DR	InterPro; IPRO07110; Ig-like.
DR	InterPro; IPR003596; Ig_v.
DR	SMART; SM00406; IGv; 1.
DR	PROSITE; PS50835; IG_LIKE; 1.
FT	NON_TER 1
FT	NON_TER 107
SEQ	SEQUENCE 107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;
Query Match 78.6%; Score 468.5; DB 2; Length 107;	
Best Local Similarity 84.8%; Pred. No. 4.6e-39;	
Matches 95; Conservative 5; Mismatches 7; Indels 5; Gaps 2;	
QY	1 DIQLTQPSLSASVGRVRTITCRASKPVDGSDSYLNWYOQGKAPKLLIYAASYLES 60
Dd	1 DIQWTQPSLSASVGRVRTITCRASSI-----SSYLNWYOQGKAPKLLIYAASSLQS 56
QY	61 GVPSRFSGSGGTDTLTITSLQPDPATYYCOQHSDPYTFGGTKVEIKR 112
Dd	57 GVPSRFSGSGGTDTLTITSLQPDPATYYCOQSY-STLTFGGTKVEIKR 107
RESULT 5	
Q6GMX0	PRELIMINARY; PRT; 236 AA.
ID	Q6GMX0
AC	Q6GMX0;
DT	05-JUL-2004 (TrEMBLrel. 27, Created)
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE	Hypothetical protein.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RN	SEQUENCE FROM N.A.
RC	TISSUP=Spleen;
RX	MEDLINE=42388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA	Krausenberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA	Alausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA	Altschul S.F., Zeeberg B., Buote K.H., Schaefer C.F., Bhat N.K.,
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA	Brownstein M.J., Usdin T.B., Toshlyufi S., Carninci P., Prange C.,
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA	Fahay J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA	Krzywinski M.I., Skalska U., Smalls D.E., Schmerch A., Schein J.E.,
RA	Jones S.J., Marra W.A.;
RT	"generation and initial analysis of more than 15,000 full-length human
RT	and mouse cDNA sequences";
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN	[2]

RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC034141; AAH34141.1; -.
 DR HSP; P01607; 1AR2.
 DR InterPro; IPR003599; Ig-like.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_C1.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF07654; C1-set; 1.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGC1; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 KW Hypothetical protein_KW
 SQ SEQUENCE 236 AA; 25603 MW; 8BC561106861213P CRC64;

Query Match 78.0%; Score 465; DB 2; Length 236;
 Best Local Similarity 82.5%; Pred. No. 2.5e-38;
 Matches 94; Conservative 5; Mismatches 11; Indels 4; Gaps 1;

Qy 1 DIQLTQSPSSLSASVGDVRVITTCRASKPVDGSDSYLNWYQKPKAPKLLIYAASYLES 60
 Db 23 DIQLTQSPSSLSASVGDVRVITTCRASKPVDGSDSYLNWYQKPKAPKLLIYAASYLES 78

Qy 61 GVPSRFGSGSGTDFLTITISLQPEDPATYQCQSHEDPYTFGGTKVEIKRTV 114
 Db 79 GVPSRFGSGSGTDFLTITISLQPEDPATYQCQSHEDPYTFGGTKVEIKRTV 132

RESULT 7

KV1W HUMAN
 ID KV1W HUMAN STANDARD; PRT; 108 AA.
 AC P01600;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Ig kappa chain V-I region Hau.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=71032830; PubMed=4097974;
 RA Watanabe S., Hilschmann N.;
 RT "The primary structure of a monoclonal kappa-type immunoglobulin L-chain of subgroup I (Bence-Jones Protein Hau): subdivision within subgroups";
 RL Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).
 CC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
 CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
 DR PIR; A01868; KIHUHU.
 DR PDB; 1F6L; X-ray; L=1-108.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR Pfam; PF00047; Ig_v.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 DR 3D-structure; Bence-Jones protein; Direct protein sequencing; Immunoglobulin V region.
 KW DOMAIN 1 23 Framework-1.
 FT DOMAIN 24 34 Complementarity-determining-1.
 FT DOMAIN 35 49 Framework-2.
 FT DOMAIN 50 56 Complementarity-determining-2.
 FT DOMAIN 57 88 Framework-3.
 FT DOMAIN 89 97 Framework-4.
 FT DOMAIN 98 107 Complementarity-determining-3.
 FT DISULFID 23 88 Framework-4.
 FT NON_TER 108 By similarity.

SQ SEQUENCE 108 AA; 11671 MW; 08D3A6160D8D0618 CRC64;
 Query Match 77.9%; Score 464; DB 1; Length 108;
 Best Local Similarity 81.2%; Pred. No. 1.3e-38;
 Matches 91; Conservative 10; Mismatches 7; Indels 4; Gaps 1;
 Qy 1 DIQLTQSPSSLSASVGDVRVITTCRASKPVDGSDSYLNWYQKPKAPKLLIYAASYLES 60
 Db 1 DIQLTQSPSSLSASVGDVRVITTCRASKPVDGSDSYLNWYQKPKAPKLLIYAASYLES 56
 Qy 61 GVPSRFGSGSGTDFLTITISLQPEDPATYQCQSHEDPYTFGGTKVEIKR 112
 Db 57 GVPSRFGSGSGTDFLTITISLQPEDPATYQCQSHEDPYTFGGTKVEIKR 108

RESULT 8

KV1E HUMAN
 ID KV1E HUMAN STANDARD; PRT; 108 AA.
 AC P01597;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ig kappa chain V-I region DEE.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=72053133; PubMed=5124396;
 RA Milstein C.P., Deverson E.V.;
 RT "The amino acid sequence of a human kappa light chain.";
 RL Biochem. J. 123:945-958(1971).
 CC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
 DR PIR; A01865; KIHUDE.
 DR HSP; P01607; 1BWV.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 KW Direct protein sequencing; Immunoglobulin V region.
 FT DOMAIN 1 23 Framework-1.
 FT DOMAIN 24 34 Complementarity-determining-1.
 FT DOMAIN 35 49 Framework-2.
 FT DOMAIN 50 56 Complementarity-determining-2.
 FT DOMAIN 57 88 Framework-3.
 FT DOMAIN 89 97 Framework-4.
 FT DISULFID 23 88 By similarity.
 FT NON_TER 108 By similarity.
 SQ SEQUENCE 108 AA; 11661 MW; BDD6E350017F1E51 CRC64;

Query Match 76.5%; Score 456; DB 1; Length 108;
 Best Local Similarity 78.6%; Pred. No. 8.2e-38;
 Matches 88; Conservative 10; Mismatches 10; Indels 4; Gaps 1;

Qy 1 DIQLTQSPSSLSASVGDVRVITTCRASKPVDGSDSYLNWYQKPKAPKLLIYAASYLES 60
 Db 1 BIZMTQSPSSLSASVGDVRVITTCRASKPVDGSDSYLNWYQKPKAPKLLIYAASYLES 56

Qy 61 GVPSRFGSGSGTDFLTITISLQPEDPATYQCQSHEDPYTFGGTKVEIKR 112
 Db 57 GVPSRFGSGSGTDFLTITISLQPEDPATYQCQSHEDPYTFGGTKVEIKR 108

RESULT 9

KV1W HUMAN
 ID KV1W HUMAN STANDARD; PRT; 129 AA.
 AC P04431;

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13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-I region Walker precursor.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85014148; PubMed=6091049;
RA Klobbeck H.G., Combrato G., Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
RL lymphoid cell lines are closely related.";
RL Nucleic Acids Res. 12:6995-7006(1984).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X00965; CAA25477.1; ALT_TERM.
DR PIR; A01883; KIHUWK.
DR HSSP; P01607; 1BWW.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR Immunoglobulin V region; Signal.
FT CHAIN 1 22 Ig kappa chain V-I region Walker.
FT DOMAIN 23 129 Framework-1.
FT DOMAIN 23 45 Complementarity-determining-1.
FT DOMAIN 46 56 Framework-2.
FT DOMAIN 57 71 Framework-3.
FT DOMAIN 72 78 Complementarity-determining-2.
FT DOMAIN 79 110 Complementarity-determining-3.
FT DOMAIN 111 119 Complementarity-determining-4.
FT DISULFID 120 129 By similarity.
FT NON TER 129 129
SQ SEQUENCE 129 AA; 14069 MW; F941FA07D4AFC2F9 CRC64;

Query Match 76.0%; Score 453; DB 1; Length 129;
Best Local Similarity 81.1%; Pred. No. 2e-37;
Matches 90; Conservative 8; Mismatches 9; Indels 4; Gaps 1;

Qy 1 DIQLTQSPSSLSASVGRVTTTCRASKPVDGSDSLNWKYQKPKAPKLIYAASLYLES 60
Db 23 DIQMTQSPSSLSASVGRVTTTCRASQSI-----SNLYNWKYQKPKAPKLIYAASLSQS 78
Qy 61 GVPGRFSGSGSGTDFTLTITSLQLPEDFATYYCQOSHEDPYTFGGQTKVEIK 111
Db 79 GVTRFSGSGSGTDFTLTITSLQLPEDSATYYCQSYSTLTITFGQTRLEIK 129

RESULT 10
KV1N HUMAN
ID KV1N HUMAN STANDARD; PRT; 108 AA.
AC P01606;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE IG kappa chain V-I region OU.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Query Match 75.5%; Score 450; DB 1; Length 108;
Best Local Similarity 71.4%; Pred. No. 3.3e-37;
Matches 80; Conservative 19; Mismatches 9; Indels 4; Gaps 1;

Qy 1 DIQLTQSPSSLSASVGRVTTTCRASKPVDGSDSLNWKYQKPKAPKLIYAASLYLES 60
Db 1 DIQMTZSPSSLSASVGRVTTTCRASZTI----SSYLBWYZZKPKAPBLIYAASBLHS 56
Qy 61 GVPGRFSGSGSGTDFTLTITSLQLPEDFATYYCQOSHEDPYTFGGQTKVEIKR 112
Db 57 GVPGRFSGSGSGTBTFTTISLSLPZBFATYYCZZSSYSSPTTFGGZTRLZIKR 108

RESULT 11
Q7Z3Y4 PRELIMINARY; PRT; 236 AA.
AC Q7Z3Y4;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal Muscle;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ussdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.U., Lu X., Gibbs R.A.,
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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=70201507; PubMed=5447531;
RA Kohler H., Shimizu A., Paul C., Putnam F.W.;
RT "Macroglobulin structure: variable sequence of light and heavy
RL chains.";
RL Science 169:56-59(1970).
CC -1- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -1- MISCELLANEOUS: This chain was isolated from a Waldenström's
CC macroglobulin.
DR PIR; A01872; KIHUOU.
DR HSSP; P01607; 1BWW.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23 Framework-1.
FT DOMAIN 24 34 Complementarity-determining-1.
FT DOMAIN 35 49 Framework-2.
FT DOMAIN 50 56 Complementarity-determining-2.
FT DOMAIN 57 88 Framework-3.
FT DOMAIN 89 97 Complementarity-determining-3.
FT DISULFID 98 107 Framework-4.
FT NON TER 108 108 By similarity.
SQ SEQUENCE 108 AA; 11777 MW; 8283D4A24105827E CRC64;

Query Match 75.5%; Score 450; DB 1; Length 108;
Best Local Similarity 71.4%; Pred. No. 3.3e-37;
Matches 80; Conservative 19; Mismatches 9; Indels 4; Gaps 1;

Qy 1 DIQLTQSPSSLSASVGRVTTTCRASKPVDGSDSLNWKYQKPKAPKLIYAASLYLES 60
Db 1 DIQMTZSPSSLSASVGRVTTTCRASZTI----SSYLBWYZZKPKAPBLIYAASBLHS 56
Qy 61 GVPGRFSGSGSGTDFTLTITSLQLPEDFATYYCQOSHEDPYTFGGQTKVEIKR 112
Db 57 GVPGRFSGSGSGTBTFTTISLSLPZBFATYYCZZSSYSSPTTFGGZTRLZIKR 108

RESULT 11
Q7Z3Y4 PRELIMINARY; PRT; 236 AA.
AC Q7Z3Y4;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal Muscle;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ussdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.U., Lu X., Gibbs R.A.,
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RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skeletal Muscle;
 RA Strausberg R.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 RL EMBL; BC005332; AAH05332.1; -.
 DR HSP; P01834; IHEZ.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig-cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF07654; C1-set; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 236 AA; 25702 MW; 7FBFE4ED23084BC6 CRC64;

 Query Match 74.8%; Score 446; DB 2; Length 236;
 Best Local Similarity 78.1%; Pred. No. 2e-36;
 Matches 89; Conservative 8; Mismatches 13; Indels 4; Gaps 1;

 QY 1 DIQLTQSPSSLSASVGDVRVTITCRASKPVDCGDSYLNWYQKPGKAPKLLIYAASYLE 60
 DB 23 DIQLTQSPSSLSASVGDVRVTITCRASQDI---SNYLAWFQKPGKAPKSLIYGASSLQS 78

 QY 61 GVPSRFGSGSGTDFTLTITSSLOPEDPATYVCOQSHEDPVTFGQGTKEIKRTV 114
 DB 79 GVQSKFGSGSGTDFTLTITSSLOPEDPATYVCOQKSYVPVTFGQGTKEIKRTV 132

 RESULT 12
 KV1B HUMAN STANDARD; PRT; 108 AA.
 ID P01594;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Ig kappa chain V-I region AU.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=72189444; PubMed=5028201;
 RA Schiechl H., Hillechmann N.;
 RT "Rule of antibody structure. The primary structure of a monoclonal
 RT immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
 RT protein Au).";
 RL Hoppe-Seyler's Z. Physiol. Chem. 353:345-370 (1972).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RX MEDLINE=77022433; PubMed=1234024;
 RA Fehllhammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,
 RA Schwager P., Steigemann W., Schramm H.J.;
 RT "The structure determination of the variable portion of the Bence-
 RT Jones protein Au.";
 RT Biophys. Struct. Mech. 1:139-146 (1975).
 CC -I- MISCELLANEOUS: The structure of the V region was determined by
 CC molecular replacement methods using the known structure of the V
 CC region of the kappa chain REL.
 CC -I- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
 CC -I- MISCELLANEOUS: This is a Bence-Jones protein.

DR PIR; A91653; KIHUAV.
 DR PDB; 1JVS; X-ray; A=1-107.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; P:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; IGV; 1.
 DR SMART; PS50835; IGV; 1.
 DR PROSITE; PS00406; IGV; 1.
 KW 3D-structure; Bence-Jones protein; Direct protein sequencing;
 KW immunoglobulin V region.
 FT DOMAIN 1 23 Framework-1.
 FT DOMAIN 24 34 Complementarity-determining-1.
 FT DOMAIN 35 49 Framework-2.
 FT DOMAIN 50 56 Complementarity-determining-2.
 FT DOMAIN 57 88 Framework-3.
 FT DOMAIN 89 97 Complementarity-determining-3.
 FT DOMAIN 98 107 Framework-4.
 FT DISULFID 23 88 By similarity.
 FT STRAND 4 5
 FT STRAND 10 13
 FT TURN 15 16
 FT STRAND 19 25
 FT TURN 30 31
 FT STRAND 33 38
 FT TURN 40 41
 FT STRAND 44 49
 FT TURN 50 52
 FT STRAND 53 54
 FT TURN 56 57
 FT TURN 60 61
 FT STRAND 62 67
 FT TURN 68 69
 FT STRAND 70 75
 FT HELIX 80 82
 FT STRAND 85 90
 FT STRAND 97 98
 FT STRAND 102 106
 FT NON TER 108 108
 SQ SEQUENCE 108 AA; 11939 MW; E8011187E6F6B9 CRC64;

 Query Match 74.7%; Score 445; DB 1; Length 108;
 Best Local Similarity 79.5%; Pred. No. 1e-36;
 Matches 89; Conservative 5; Mismatches 14; Indels 4; Gaps 1;

 QY 1 DIQLTQSPSSLSASVGDVRVTITCRASKPVDCGDSYLNWYQKPGKAPKLLIYAASYLE 60
 DB 1 DIQLTQSPSSLSASVGDVRVTITCRASQDI---SDYLNWYQKPGKAPKLLIYDASNLES 56

 QY 61 GVPSRFGSGSGTDFTLTITSSLOPEDPATYVCOQSHEDPVTFGQGTKEIKR 112
 DB 57 GVPSRFGSGSGTDFTLTITSSLOPEDPATYVCOQYDYLPTWTFQGTKEIKR 108

 RESULT 13
 KV1V HUMAN STANDARD; PRT; 108 AA.
 ID P04430;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ig kappa chain V-I region BAN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=86174817; PubMed=3083240; DOI=10.1016/0161-5890(86)90173-2;
 RA Dwyer F.E., O'Connor T.P., Benson M.D.;
 RT "Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";
 RL Mol. Immunol. 23:73-78 (1986).

```
DR PIR: A01878; K1HUBN.
DR HSSP: P80362; 1WTL.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; P:antigen binding; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003596; IG_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
KW Amyloid; Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON_TER 1 108
FT NON_TER 107 108
SQ SEQUENCE 108 AA; 11840 MW; CD3FD944FE96FD37 CRC64;

Query Match 74.7%; Score 445; DB 1; Length 108;
Best Local Similarity 79.5%; Pred. No. 1e-36;
Matches 89; Conservative 8; Mismatches 11; Indels 4; Gaps 1;

Qy 1 DIQLTQSPSSLSASVGDRTVITTCRAKPKVDGEGSYLNWYQKPKAPKLLIYAASYLES 60
Db 1 DIQLTQSPSSLSASVGDRTVITTCRASQSV----YNYVAFQKPKAPKPSLIYDASTLQS 56

Qy 61 GVPFRFSGSGSGTDTLTITSLQPEDFATYYCQOSHEDPYTFGQTKVEIKR 112
Db 57 GVPNFTGSGSGTDTLTITSLQPEDFATYYCQYNSPYTFGQTKVQIKR 108

RESULT 14
Q9UL81 PRELIMINARY; PRT; 107 AA.
AC Q9UL81
DR 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035033; AAD56269.1; -.
DR HSSP: P01607; 1BW.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003596; IG_v.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
FT NON_TER 1 107
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match 74.4%; Score 443.5; DB 2; Length 107;
Best Local Similarity 79.5%; Pred. No. 1.5e-36;
Matches 89; Conservative 8; Mismatches 10; Indels 5; Gaps 2;

Qy 1 DIQLTQSPSSLSASVGDRTVITTCRAKPKVDGEGSYLNWYQKPKAPKLLIYAASYLES 60
Db 1 DIQLTQSPSSLSASVGDRTVITTCRASQSI-----SNYLNWYQKPKAPKLLIYAASLSQS 56

us-10-791-619-8.rup

Qy 61 GVPFRFSGSGSGTDTLTITSLQPEDFATYYCQOSHEDPYTFGQTKVEIKR 112
Db 57 GVPFRFSGSGSGTDTLTITSLQPEDFATYYCQOSY-SALTFGPKTKVDIR 107

RESULT 15
KVIM_HUMAN STANDARD; PRT; 108 AA.
AC KVIM_HUMAN
DR 21-JUL-1996 (Rel. 01, Created)
DT 21-JUL-1996 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-I region Lay.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=77038198; PubMed=824717;
RA Capra J.D., Klapper D.G.;
RT "Complete amino acid sequence of the variable domains of two human IgM
RT anti-gamma globulins (Lay/Pom) with shared idiotypic specificities.";
RL Scand. J. Immunol. 5:677-684(1976).
CC -!- MISCELLANEOUS: The second and third hypervariable regions of this
CC chain are identical with those of the human POM V-III kappa chain,
CC with which it shares certain idiotypic determinants.
CC -!- MISCELLANEOUS: This chain was isolated from an IgM with anti-gamma
CC globulin activity.
CC PIR: A01871; K1HULY.
DR HSSP: P01607; 1BW.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; P:antigen binding; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003596; IG_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON_TER 1 108
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11834 MW; 739993A95431434A CRC64;

Query Match 74.3%; Score 443; DB 1; Length 108;
Best Local Similarity 78.6%; Pred. No. 1.6e-36;
Matches 88; Conservative 8; Mismatches 12; Indels 4; Gaps 1;

Qy 1 DIQLTQSPSSLSASVGDRTVITTCRAKPKVDGEGSYLNWYQKPKAPKLLIYAASYLES 60
Db 1 DIQMTQSPSSLSASVGDRTVITTCASQNV----NAYLNWYQKPKAPKLLIYGASTREA 56

Qy 61 GVPFRFSGSGSGTDTLTITSLQPEDFATYYCQOSHEDPYTFGQTKVEIKR 112
Db 57 GVPFRFSGSGSGTDTLTITSLQPEDIATYYCQYNNWPPPTFGQTKVEIKR 108

Search completed: June 3, 2005, 09:16:13
Job time : 33.7497 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 3, 2005, 08:29:47 ; Search time 37.3502 Seconds
(without alignments)
1180.467 Million cell updates/sec

Title: US-10-791-619-8
Perfect score: 596
Sequence: 1 DIQLTQSPSSLSASVGRVLT.....SHEDPYTFGQGTKEIKRTV 114

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_16Dec04:.*
1: geneseq1980s:.*
2: geneseq1990s:.*
3: geneseq2000s:.*
4: geneseq2001s:.*
5: geneseq2002s:.*
6: geneseq2003as:.*
7: geneseq2003bs:.*
8: geneseq2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	596	100.0	114	4	AAB76942 Variable
2	596	100.0	114	8	ADN07029 Anti-IgE
3	596	100.0	218	2	Aaw95664 Mus muscu
4	596	100.0	218	2	Aaw95669 Mus muscu
5	596	100.0	218	4	AAB47087 Anti-IgE
6	596	100.0	218	4	AAB76949 Full leng
7	596	100.0	218	4	AAB76951 Full leng
8	596	100.0	218	4	AAB76953 Variable
9	596	100.0	218	4	AAB76958 Variable
10	596	100.0	218	8	ADN07045 Anti-IgE
11	596	100.0	218	8	ADN07036 Anti-IgE
12	596	100.0	218	8	ADN07038 Anti-IgE
13	596	100.0	218	8	ADN07040 Anti-IgE
14	594	99.7	114	2	Aaw95653 Mus muscu
15	594	99.7	218	2	Aaw95660 Mus muscu
16	594	99.7	218	2	Aaw95662 Mus muscu
17	594	99.7	218	2	AAY50030 Human E27
18	594	99.7	218	3	AAB07472 Amino aci
19	594	99.7	218	4	AAB74211 E27 anti-
20	594	99.7	218	6	ABU62797 E27 anti-
21	594	99.7	218	7	ADP69597 Human ant
22	594	99.7	218	7	ADP29038 Anti-IgE
23	587	98.5	248	2	Aaw95668 Mus muscu
24	587	98.5	248	2	Aaw95667 Mus muscu
25	587	98.5	248	4	AAB76957 SfV fragm

26	587	98.5	248	4	AAB76956	Aab76956 SfV fragm
27	587	98.5	248	8	ADN07044	Adn07044 Anti-IgE
28	587	98.5	248	8	ADN07043	Adn07043 Anti-IgE
29	575	96.5	114	4	AAB76943	Aab76943 Variable
30	575	96.5	114	8	ADN07030	Adn07030 Anti-IgE
31	575	96.5	219	8	ADN07066	Adn07066 F(ab)-pha
32	573	96.1	114	2	AAW95654	Aaw95654 Mus muscu
33	570	95.6	114	2	AAW95655	Aaw95655 Mus muscu
34	570	95.6	114	4	AAB76944	Aab76944 Variable
35	570	95.6	114	8	ADN07031	Adn07031 Anti-IgE
36	570	95.6	218	2	AAW95658	Aaw95658 Mus muscu
37	570	95.6	218	3	AAW85200	Aaw85200 Light cha
38	570	95.6	218	4	AAB76947	Aab76947 Full vari
39	570	95.6	218	8	ADN07034	Adn07034 Anti-IgE
40	570	95.6	241	8	ADQ90719	Adq90719 Anti-IgE
41	570	95.6	241	8	ADQ90717	Adq90717 Anti-IgE
42	563	94.5	218	2	AAK33312	Aak33312 Humanised
43	556	93.3	111	2	AAW95651	Aaw95651 Mus muscu
44	556	93.3	111	4	AAB76940	Aab76940 Variable
45	556	93.3	111	8	ADN07027	Adn07027 Murine an

ALIGNMENTS

RESULT 1
AAB76942
ID AAB76942 standard; protein; 114 AA.
XX
AC AAB76942;
XX
DT 17-APR-2001 (first entry)
XX
DE Variable light chain sequence of e26 and e27 SEQ ID 8.
XX
KW Antibody; antiasthmatic; antiallergic; ophthalmological; dermatological;
KW antiinflammatory; Ig E; immunoglobulin E; asthma; allergic rhinitis;
KW conjunctivitis; eczema; urticaria; food allergy.
XX
OS Synthetic.
XX
PN US6172213-B1.
XX
PD 09-JAN-2001.
XX
PF 30-JUN-1998; 98US-00109207.
XX
PR 02-JUL-1997; 97US-0051554P.
XX
PA (GETH) GENENTECH INC.
XX
PI Lowman HB, Presta LG, Jardieu PM, Lowe J;
XX
DR WPI; 2001-122353/13.
XX
PT New nucleic acid encoding anti-immunoglobulin E antibody with improved
PT properties, produced by substituting aspartyl residues in unimproved
PT immunoglobulin E prone to isomerization by other residues by affinity
PT maturation with phage display.
XX
PS Disclosure; Fig 2; 87pp; English.

XX
CC This invention relates to a nucleotide sequence encoding an antibody with improved anti-IgE antibody activity. The antibody has improved action due to a process comprising, a) identifying aspartyl residues prone to isomerisation in unimproved anti-IgE (immunoglobulin E) antibody; b) substituting alternative residues to create candidate molecules, and c) selecting those candidate molecules which display affinity against the target molecule. Use of the antibody results in antiasthmatic; antiallergic; ophthalmological; dermatological and antiinflammatory activity. The antibodies are useful for treating IgE-mediated disorders such as asthma, allergic rhinitis, conjunctivitis, eczema, urticaria and food allergies. The mutant antibodies produced by the above mentioned

CC nucleic acids may also be used as affinity purification agents and in
 CC diagnostic assays for detecting the expression of an antigen of interest
 CC in specific cell, tissues or serum. Amino acid sequences AAB76936-
 CC AAB76960 represent fragments of anti-IgE antibodies of the invention.
 CC Polynucleotide sequence AAF69253 represents an expression plasmid used in
 CC the course of the invention, and oligonucleotides AAF69254 - AAF69271 are
 CC used in the generation of affinity improved anti-IgE antibodies
 XX
 SQ Sequence 114 AA;

Query Match 100.0%; Score 596; DB 4; Length 114;
 Best Local Similarity 100.0%; Pred. No. 1.2e-35;
 Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DIQLTQSPSSLSASVGRVITTCRASKPVDGSDSYLNWYQKPGKAPKLLIYAASYLE 60
 Db 1 DIQLTQSPSSLSASVGRVITTCRASKPVDGSDSYLNWYQKPGKAPKLLIYAASYLE 60
 QY 61 GVPFRSGSGSGDTFTLTSSLPEDPATYCCQSHEDPYTFGGTKVEIKRTV 114
 Db 61 GVPFRSGSGSGDTFTLTSSLPEDPATYCCQSHEDPYTFGGTKVEIKRTV 114

RESULT 2
 ADN07029
 ID ADN07029 standard; protein; 114 AA.

AC ADN07029;
 XX
 DT 01-JUL-2004 (first entry)
 XX
 DE Anti-IgE antibody e26 and e27 variable light chain domain (VL).
 XX
 KW Anti-IgE antibody; immunosuppressive agent; IgE-mediated disorder;
 KW therapy; atopic allergy; anaphylactic hypersensitivity; asthma;
 KW allergic rhinitis; conjunctivitis; eczema; urticaria; food allergy;
 KW variable light chain domain; VL.
 XX
 OS Unidentified.

XX
 FH Key Location/Qualifiers
 FT Region 24..40
 FT /label= CDR-L1
 FT Region 54..60
 FT /label= CDR-L2
 FT Region 93..100
 FT /label= CDR-L3
 XX

US6723833-B1.

20-APR-2004.

17-NOV-2000; 2000US-00716028.

02-JUL-1997; 97US-0051554P.

30-JUN-1998; 98US-00109207.

(GETH) GENENTECH INC.

Lowman HB, Presta LG, Jardieu PM, Lowe J;

WPI; 2004-326922/30.

PT New composition of an improved anti-IgE antibody or IgE binding fragment,
 PT useful for treating IgE-mediated diseases, e.g. atopic allergy, asthma,
 PT conjunctivitis, eczema, urticaria or food allergies.

XX Disclosure; SEQ ID NO 8; 89pp; English.

XX The invention relates to therapeutic compositions comprising anti-IgE
 CC antibody or IgE binding fragment in combination with an adjunct
 CC immunosuppressive agent. The composition is useful for treating IgE-
 CC mediated disorders. The disorders include atopic allergy associated with

CC anaphylactic hypersensitivity and asthma, allergic rhinitis and
 CC conjunctivitis, eczema, urticaria and food allergies. The present
 CC sequence is an anti-IgE antibody variable light chain domain (VL).
 XX
 SQ Sequence 114 AA;

Query Match 100.0%; Score 596; DB 8; Length 114;
 Best Local Similarity 100.0%; Pred. No. 1.2e-35;
 Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGRVITTCRASKPVDGSDSYLNWYQKPGKAPKLLIYAASYLE 60
 Db 1 DIQLTQSPSSLSASVGRVITTCRASKPVDGSDSYLNWYQKPGKAPKLLIYAASYLE 60

QY 61 GVPFRSGSGSGDTFTLTSSLPEDPATYCCQSHEDPYTFGGTKVEIKRTV 114
 Db 61 GVPFRSGSGSGDTFTLTSSLPEDPATYCCQSHEDPYTFGGTKVEIKRTV 114

RESULT 3
 AAW95664
 ID AAW95664 standard; protein; 218 AA.

AC AAW95664;

XX 08-JUN-1999 (first entry)

DE Mus musculus anti-IgE e26 & e27 variable light chain Fab fragment.

XX Variable light Fab fragment; antibody; anti-IgE; reduction; prevention;
 KW histamine; production; hypersensitivity; allergen; anaphylaxis;
 KW atopic allergy; asthma; allergic rhinitis; conjunctivitis; hay fever;
 KW eczema; anaphylactic shock; urticaria; IgE.

OS Mus musculus.

XX WO9901556-A2.

XX 14-JAN-1999.

XX 30-JUN-1998; 98WO-US013410.

XX 02-JUL-1997; 97US-00887352.

XX (GETH) GENENTECH INC.

PI Lowman HB, Presta LG, Jardieu PM, Lowe J;

XX WPI; 1999-106057/09.

XX Improving affinity of polypeptides, particularly anti-IgE antibodies - by
 PT identifying aspartyl residues which undergo isomerisation and
 PT substituting alternative residues and screening for affinity against the
 PT target.

XX Disclosure; Page 99-100; 129pp; English.

XX The sequence is that of the variable light Fab fragment of e26 and e27.
 CC It was used as part of a method to improve the affinity of anti-IgE
 CC antibodies such as e26 and e27. The e26 and e27 antibodies can be used
 CC for reducing or preventing IgE mediated production of histamine in a
 CC mammal. They can be used for treating a disorder mediated by IgE such as
 CC hypersensitivity, atopic allergy, asthma, allergic rhinitis,
 CC conjunctivitis, hay fever, eczema, anaphylactic shock and urticaria. The
 CC antibodies can also be used for affinity purification, detection and
 CC diagnosis

XX Sequence 218 AA;

Query Match 100.0%; Score 596; DB 2; Length 218;
 Best Local Similarity 100.0%; Pred. No. 2.1e-35;
 Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTVITTCRASKEVDGSDSYLNWYQOKPKAPKLLIYAASYLE 60
 Db 1 DIQLTQSPSSLSASVGDRTVITTCRASKEVDGSDSYLNWYQOKPKAPKLLIYAASYLE 60

QY 61 GVPFRFSGSGSGTDFTLTISSLPQEDFATYTCQSHEDPYTFGQGTKEIKRTV 114
 Db 61 GVPFRFSGSGSGTDFTLTISSLPQEDFATYTCQSHEDPYTFGQGTKEIKRTV 114

RESULT 4
 AAW95669
 ID AAW95669 standard; protein; 218 AA.
 XX
 AC AAW95669;
 XX
 DT 08-JUN-1999 (first entry)
 XX
 DE Mus musculus anti-IgE e26 & e27 variable light chain F(ab)'2 fragment.
 XX
 KW Variable light chain; IgE; antibody; anti-IgE; reduction; prevention;
 KW histamine; production; hypersensitivity; allergen; anaphylaxis;
 KW atopic allergy; asthma; allergic rhinitis; conjunctivitis; hay fever;
 KW eczema; anaphylactic shock; urticaria; F(ab)'2 fragment.
 XX
 OS Mus musculus.
 XX
 FN WO9901556-A2.
 XX
 PD 14-JAN-1999.
 XX
 PF 30-JUN-1998; 98WO-US013410.
 XX
 FR 02-JUL-1997; 97US-00887352.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Lowman HB, Presta LG, Jardieu PM, Lowe J;
 XX
 DR WPI; 1999-106057/09.
 XX
 PT Improving affinity of polypeptides, particularly anti-IgE antibodies - by
 PT identifying aspartyl residues which undergo isomerisation and
 PT substituting alternative residues and screening for affinity against the
 PT target.
 XX
 PS Disclosure; Page 104; 129pp; English.
 XX
 CC The sequence is that of the variable light chain F(ab)'2 fragment of e26
 CC and e27. It was used as part of a method to improve the affinity of anti-
 CC IgE antibodies such as e26 and e27. The e26 and e27 antibodies can be
 CC used for reducing or preventing IgE mediated production of histamine in a
 CC mammal. They can be used for treating a disorder mediated by IgE such as
 CC hypersensitivity, atopic allergy, asthma, allergic rhinitis,
 CC conjunctivitis, hay fever, eczema, anaphylactic shock and urticaria. The
 CC antibodies can also be used for affinity purification, detection and
 CC diagnosis
 XX
 SQ Sequence 218 AA;
 Query Match 100.0%; Score 596; DB 2; Length 218;
 Best Local Similarity 100.0%; Pred. No. 2.1e-35;
 Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTVITTCRASKEVDGSDSYLNWYQOKPKAPKLLIYAASYLE 60
 Db 1 DIQLTQSPSSLSASVGDRTVITTCRASKEVDGSDSYLNWYQOKPKAPKLLIYAASYLE 60

QY 61 GVPFRFSGSGSGTDFTLTISSLPQEDFATYTCQSHEDPYTFGQGTKEIKRTV 114
 Db 61 GVPFRFSGSGSGTDFTLTISSLPQEDFATYTCQSHEDPYTFGQGTKEIKRTV 114

RESULT 5
 AAW76949
 ID AAW76949 standard; protein; 218 AA.
 XX
 AC AAW76949;

AAAB47087
 ID AAAB47087 standard; protein; 218 AA.
 XX
 AC AAAB47087;
 XX
 DT 11-SEP-2003 (revised)
 DT 08-MAY-2001 (first entry)
 XX
 DE Anti-IgE antibody, E26, light chain.
 XX
 KW Light chain; heavy chain; anti-IgE antibody; E26; transfection;
 KW green fluorescent protein; GFP; promoter; expression.
 XX
 OS Homo sapiens.
 OS Mus musculus.
 OS Chimeric.
 XX
 PN WO200104306-A1.
 XX
 PD 18-JAN-2001.
 XX
 PF 11-JUL-2000; 2000WO-US018841.
 XX
 PR 12-JUL-1999; 99US-0143360P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Chisholm V, Crowley CW, Krummen LA, Meng YG;
 XX
 DR WPI; 2001-138352/14.
 XX
 PT Novel polynucleotide construct for screening and obtaining cells
 PT expressing high levels of desired protein, comprises amplifiable
 PT selectable gene, fluorescent protein gene and sequence encoding desired
 PT product.
 XX
 PS Disclosure; Fig 13A; 75pp; English.
 XX
 CC The sequences given in AAAB47087-88 represent the light and heavy chains
 CC of the anti-IgE antibody, E26. These sequences were expressed by the
 CC construct of the invention, which comprises an amplifiable selectable
 CC gene, a green fluorescent protein gene (GFP), and a selected sequence
 CC encoding a desired product, which is operably linked to either the
 CC amplifiable selectable gene or to the GFP gene, and to a promoter.
 CC Constructs such as this, are useful for producing a desired product by
 CC introduction into a suitable eukaryotic cell, culturing the resultant
 CC eukaryotic cell under conditions so as to express the desired product,
 CC and recovering the desired product from the culture medium. The
 CC constructs are efficient for identifying and selecting for stable
 CC eukaryotic cells expressing high levels of a desired product. They are
 CC suitable for earlier and faster screening of transfected cells. (Updated
 CC on 11-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 218 AA;
 Query Match 100.0%; Score 596; DB 4; Length 218;
 Best Local Similarity 100.0%; Pred. No. 2.1e-35;
 Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLSASVGDRTVITTCRASKEVDGSDSYLNWYQOKPKAPKLLIYAASYLE 60
 Db 1 DIQLTQSPSSLSASVGDRTVITTCRASKEVDGSDSYLNWYQOKPKAPKLLIYAASYLE 60

QY 61 GVPFRFSGSGSGTDFTLTISSLPQEDFATYTCQSHEDPYTFGQGTKEIKRTV 114
 Db 61 GVPFRFSGSGSGTDFTLTISSLPQEDFATYTCQSHEDPYTFGQGTKEIKRTV 114

RESULT 6
 AAB76949
 ID AAB76949 standard; protein; 218 AA.
 XX
 AC AAB76949;

```

XX DT 17-APR-2001 (first entry)
XX DE Full length light chain sequence of e26 SEQ ID 15.
XX KW Antibody; antiasthmatic; antiallergic; ophthalmological; dermatological;
XX KW antiinflammatory; Ig E; immunoglobulin E; asthma; allergic rhinitis;
XX KW conjunctivitis; eczema; urticaria; food allergy.
XX OS Synthetic.
XX PN US6172213-B1.
XX PD 09-JAN-2001.
XX PF 30-JUN-1998; 98US-00109207.
XX PR 02-JUL-1997; 97US-0051554P.
XX PA (GETH ) GENENTECH INC.
XX PI Lowman HB, Presta LG, Jardieu PM, Lowe J;
XX DR WPI; 2001-122353/13.
XX PT New nucleic acid encoding anti-immunoglobulin E antibody with improved
XX PT properties, produced by substituting aspartyl residues in unimproved
XX PT immunoglobulin E prone to isomerization by other residues by affinity
XX PT maturation with phage display.
XX PS Claim 2; Fig 12; 87pp; English.
XX CC This invention relates to a nucleotide sequence encoding an antibody with
XX CC improved anti-IgE antibody activity. The antibody has improved action due
XX CC to a process comprising, a) identifying aspartyl residues prone to
XX CC isomerisation in unimproved anti-IgE (immunoglobulin E) antibody; b)
XX CC substituting alternative residues to create candidate molecules, and c)
XX CC selecting those candidate molecules which display affinity against the
XX CC target molecule. Use of the antibody results in antiasthmatic;
XX CC antiallergic; ophthalmological; dermatological and antiinflammatory
XX CC activity. The antibodies are useful for treating IgE-mediated disorders
XX CC such as asthma, allergic rhinitis, conjunctivitis, eczema, urticaria and
XX CC food allergies. The mutant antibodies produced by the above mentioned
XX CC nucleic acids may also be used as affinity purification agents and in
XX CC diagnostic assays for detecting the expression of an antigen of interest
XX CC in specific cell, tissues or serum. Amino acid sequences AAB76936-
XX CC AAB76960 represent fragments of anti-IgE antibodies of the invention.
XX CC Polynucleotide sequence AAF69253 represents an expression plasmid used in
XX CC the course of the invention, and oligonucleotides AAF69254 - AAF69271 are
XX CC used in the generation of affinity improved anti-IgE antibodies
XX SQ Sequence 218 AA;

Query Match 100.0%; Score 596; DB 4; Length 218;
Best Local Similarity 100.0%; Pred. No. 2.1e-35;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTQSPSLASVGRVITTCRASPVDGSDSYLNWYQKPGKAPKLLIYAASYLE 60
DB 1 DIQLTQSPSLASVGRVITTCRASPVDGSDSYLNWYQKPGKAPKLLIYAASYLE 60
QY 61 GVPSRFGSGSGDTFTLTISLQPEDPATYCCQSHEDPTFFGGTKVEIKRTV 114
DB 61 GVPSRFGSGSGDTFTLTISLQPEDPATYCCQSHEDPTFFGGTKVEIKRTV 114

RESULT 7
AAB76951
ID AAB76951 standard; protein; 218 AA.
AC AAB76951;
XX DT 17-APR-2001 (first entry)

```

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XX DE Full length light chain sequence of e27 SEQ ID 17.
XX KW Antibody; antiasthmatic; antiallergic; ophthalmological; dermatological;
XX KW antiinflammatory; Ig E; immunoglobulin E; asthma; allergic rhinitis;
XX KW conjunctivitis; eczema; urticaria; food allergy.
XX OS Synthetic.
XX PN US6172213-B1.
XX PD 09-JAN-2001.
XX PF 30-JUN-1998; 98US-00109207.
XX PR 02-JUL-1997; 97US-0051554P.
XX PA (GETH ) GENENTECH INC.
XX PI Lowman HB, Presta LG, Jardieu PM, Lowe J;
XX DR WPI; 2001-122353/13.
XX PT New nucleic acid encoding anti-immunoglobulin E antibody with improved
XX PT properties, produced by substituting aspartyl residues in unimproved
XX PT immunoglobulin E prone to isomerization by other residues by affinity
XX PT maturation with phage display.
XX PS Claim 4; Fig 12; 87pp; English.
XX CC This invention relates to a nucleotide sequence encoding an antibody with
XX CC improved anti-IgE antibody activity. The antibody has improved action due
XX CC to a process comprising, a) identifying aspartyl residues prone to
XX CC isomerisation in unimproved anti-IgE (immunoglobulin E) antibody; b)
XX CC substituting alternative residues to create candidate molecules, and c)
XX CC selecting those candidate molecules which display affinity against the
XX CC target molecule. Use of the antibody results in antiasthmatic;
XX CC antiallergic; ophthalmological; dermatological and antiinflammatory
XX CC activity. The antibodies are useful for treating IgE-mediated disorders
XX CC such as asthma, allergic rhinitis, conjunctivitis, eczema, urticaria and
XX CC food allergies. The mutant antibodies produced by the above mentioned
XX CC nucleic acids may also be used as affinity purification agents and in
XX CC diagnostic assays for detecting the expression of an antigen of interest
XX CC in specific cell, tissues or serum. Amino acid sequences AAB76936-
XX CC AAB76960 represent fragments of anti-IgE antibodies of the invention.
XX CC Polynucleotide sequence AAF69253 represents an expression plasmid used in
XX CC the course of the invention, and oligonucleotides AAF69254 - AAF69271 are
XX CC used in the generation of affinity improved anti-IgE antibodies
XX SQ Sequence 218 AA;

Query Match 100.0%; Score 596; DB 4; Length 218;
Best Local Similarity 100.0%; Pred. No. 2.1e-35;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTQSPSLASVGRVITTCRASPVDGSDSYLNWYQKPGKAPKLLIYAASYLE 60
DB 1 DIQLTQSPSLASVGRVITTCRASPVDGSDSYLNWYQKPGKAPKLLIYAASYLE 60
QY 61 GVPSRFGSGSGDTFTLTISLQPEDPATYCCQSHEDPTFFGGTKVEIKRTV 114
DB 61 GVPSRFGSGSGDTFTLTISLQPEDPATYCCQSHEDPTFFGGTKVEIKRTV 114

RESULT 8
AAB76953
ID AAB76953 standard; protein; 218 AA.
AC AAB76953;
XX DT 17-APR-2001 (first entry)
XX DE Variable light chain Fab fragment of e26 and e27 SEQ ID 19.

```

XX	Antibody; antiasthmatic; antiallergic; ophthalmological; dermatological;
KW	antiinflammatory; Ig E; immunoglobulin E; asthma; allergic rhinitis;
KW	conjunctivitis; eczema; urticaria; food allergy.
XX	
OS	Synthetic.
XX	
PN	US6172213-B1.
XX	
PD	09-JAN-2001.
XX	
XX	30-JUN-1998; 98US-00109207.
PF	
XX	
XX	02-JUL-1997; 97US-0051554P.
PR	
XX	(GETH) GENENTECH INC.
PA	
XX	
PI	Lowman HB, Presta LG, Jardieu PM, Lowe J;
XX	
XX	WFI; 2001-122353/13.
DR	
XX	
PT	New nucleic acid encoding anti-immunoglobulin E antibody with improved
PT	properties, produced by substituting aspartyl residues in unimproved
PT	immunoglobulin E prone to isomerization by other residues by affinity
PT	maturation with phage display.
XX	
PS	Claim 1; Fig 13; 87pp; English.
XX	
CC	This invention relates to a nucleotide sequence encoding an antibody with
CC	improved anti-IgE antibody activity. The antibody has improved action due
CC	to a process comprising, a) identifying aspartyl residues prone to
CC	isomerisation in unimproved anti-IgE (immunoglobulin E) antibody; b)
CC	substituting alternative residues to create candidate molecules, and c)
CC	selecting those candidate molecules which display affinity against the
CC	target molecule. Use of the antibody results in antiasthmatic;
CC	antiallergic; ophthalmological; dermatological and antiinflammatory
CC	activity. The antibodies are useful for treating Igs-mediated disorders
CC	such as asthma, allergic rhinitis, conjunctivitis, eczema, urticaria and
CC	food allergies. The mutant antibodies produced by the above mentioned
CC	nucleic acids may also be used as affinity purification agents and in
CC	diagnostic assays for detecting the expression of an antigen of interest
CC	in specific cell, tissues or serum. Amino acid sequences AAB76936-
CC	AAB76960 represent fragments of anti-IgE antibodies of the invention.
CC	Polynucleotide sequence AAF69253 represents an expression plasmid used in
CC	the course of the invention, and oligonucleotides AAF69254 - AAF69271 are
CC	used in the generation of affinity improved anti-IgE antibodies
XX	
SQ	Sequence 218 AA;
	Query Match 100.0%; Score 596; DB 4; Length 218;
	Best Local Similarity 100.0%; Pred. No. 2.1e-35;
	Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Qy	1 DIQLTQSPSSLSASVGDRTVITTCRAKPKVDGSDSYLNWYQOKPKAPKLLIYAASYLES 60
Db	1 DIQLTQSPSSLSASVGDRTVITTCRAKPKVDGSDSYLNWYQOKPKAPKLLIYAASYLES 60
Qy	61 GVPKRSFGSGSGTDFLLTISLQPEDPFTATYCCQSHEDPYTFGQGTKEVEIKRTV 114
Db	61 GVPKRSFGSGSGTDFLLTISLQPEDPFTATYCCQSHEDPYTFGQGTKEVEIKRTV 114
RESULT 9	
AAAB76958	
ID	AAAB76958 standard; protein; 218 AA.
XX	
AC	AAAB76958;
XX	
DT	17-APR-2001 (first entry)
XX	
DE	Variable light chain F(ab)'2 fragment of e26 and e27 SEQ ID 24.
XX	
KW	Antibody; antiasthmatic; antiallergic; ophthalmological; dermatological;

KW	antiinflammatory; Ig E; immunoglobulin E; asthma; allergic rhinitis;
KW	conjunctivitis; eczema; urticaria; food allergy.
XX	
OS	Synthetic.
XX	
PN	US6172213-B1.
XX	
PD	09-JAN-2001.
XX	
PF	30-JUN-1998; 98US-00109207.
XX	
PR	02-JUL-1997; 97US-0051554P.
XX	
PA	(GETH) GENENTECH INC.
XX	
PI	Lowman HB, Presta LG, Jardieu PM, Lowe J;
XX	
DR	WPI; 2001-122353/13.
XX	
PT	New nucleic acid encoding anti-immunoglobulin E antibody with improved
PT	properties, produced by substituting aspartyl residues in unimproved
PT	immunoglobulin E prone to isomerization by other residues by affinity
PT	maturation with phage display.
XX	
PS	Claim 1; Fig 15; 87pp; English.
XX	
CC	This invention relates to a nucleotide sequence encoding an antibody with
CC	improved anti-IgE antibody activity. The antibody has improved action due
CC	to a process comprising, a) identifying aspartyl residues prone to
CC	isomerisation in unimproved anti-IgE (immunoglobulin E) antibody; b)
CC	substituting alternative residues to create candidate molecules, and c)
CC	selecting those candidate molecules which display affinity against the
CC	target molecule. Use of the antibody results in antiasthmatic;
CC	anti-allergic; ophthalmological; dermatological and antiinflammatory
CC	activity. The antibodies are useful for treating IgE-mediated disorders
CC	such as asthma, allergic rhinitis, conjunctivitis, eczema, urticaria and
CC	food allergies. The mutant antibodies produced by the above mentioned
CC	nucleic acids may also be used as affinity purification agents and in
CC	diagnostic assays for detecting the expression of an antigen of interest
CC	in specific cell, tissues or serum. Amino acid sequences AAB76936-
CC	AA876960 represent fragments of anti-IgE antibodies of the invention.
CC	Polynucleotide sequence AAF69253 represents an expression plasmid used in
CC	the course of the invention, and oligonucleotides AAF69254 - AAF69271 are
CC	used in the generation of affinity improved anti-IgE antibodies
XX	
SQ	Sequence 218 AA;
	Query Match 100.0%; Score 596; DB 4; Length 218;
	Best Local Similarity 100.0%; Pred. No. 2.4e-35;
	Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY	1 DIQLTQSPSSLASVGRVVTITCRASKPVDGSDYLNWYQOKPKAPKLLIYAASYLES 60
Db	1 DIQLTQSPSSLASVGRVVTITCRASKPVDGSDYLNWYQOKPKAPKLLIYAASYLES 60
QY	61 GVPKRFSGSGGTDTFTLTISQLQPEDPATYTCQSHEDPYTFGQGTKEIKRTV 114
Db	61 GVPKRFSGSGGTDTFTLTISQLQPEDPATYTCQSHEDPYTFGQGTKEIKRTV 114
RESULT 10	
ADN07045	
ADN07045	standard; protein; 218 AA.
XX	
AC	ADN07045;
XX	
DT	01-JUL-2004 (first entry)
XX	
DE	Anti-IgE antibody e26 and e27 variable light (VL) F(ab)' 2 fragment.
XX	
KW	Anti-IgE antibody; immunosuppressive agent; IgE-mediated disorder;
KW	therapy; atopic allergy; anaphylactic hypersensitivity; asthma;
KW	allergic rhinitis; conjunctivitis; eczema; urticaria; food allergy;

KW variable light chain; VL.
 OS Unidentified.
 XX
 PN US6723833-B1.
 XX
 PD 20-APR-2004.
 XX
 XX 17-NOV-2000; 2000US-00716028.
 XX
 XX 02-JUL-1997; 97US-0051554P.
 PR 30-JUN-1998; 98US-00109207.
 XX
 XX (GETH) GENENTECH INC.
 PA
 XX Lowman HB, Presta LG, Jardieu PM, Lowe J;
 PI
 XX WPI; 2004-326922/30.
 DR
 XX New composition of an improved anti-IgE antibody or IgE binding fragment,
 PT useful for treating IgE-mediated diseases, e.g. atopic allergy, asthma,
 PT conjunctivitis, eczema, urticaria or food allergies.
 XX
 XX Claim 7; SEQ ID NO 24; 89pp; English.
 PS
 XX The invention relates to therapeutic compositions comprising anti-IgE
 CC antibody or IgE binding fragment in combination with an adjunct
 CC immunosuppressive agent. The composition is useful for treating IgE-
 CC mediated disorders. The disorders include atopic allergy associated with
 CC anaphylactic hypersensitivity and asthma, allergic rhinitis and
 CC conjunctivitis, eczema, urticaria and food allergies. The present
 CC sequence is an anti-IgE antibody variable light chain (VL) F(ab)' 2
 CC fragment.
 XX
 XX Sequence 218 AA;
 SQ

Query Match 100.0%; Score 596; DB 8; Length 218;
 Best Local Similarity 100.0%; Pred. No. 2.1e-35;
 Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DIQLTQSPSLASVGRVTITCRASKPVDGSDSYLNWYQQKPGKAPKLLIYAASYLE 60
 DB 1 DIQLTQSPSLASVGRVTITCRASKPVDGSDSYLNWYQQKPGKAPKLLIYAASYLE 60
 QY 61 GVPSRFGSGSGTDFLTITSSLPQEDPATYVCOQSHEDPYTFGGTKVEIKRTV 114
 DB 61 GVPSRFGSGSGTDFLTITSSLPQEDPATYVCOQSHEDPYTFGGTKVEIKRTV 114

RESULT 11
 ADN07036
 ID ADN07036 standard; protein; 218 AA.
 AC ADN07036;
 XX
 DT 01-JUL-2004 (first entry)
 DE Anti-IgE antibody e26 full length variable light chain (VL).
 XX
 KW Anti-IgE antibody; immunosuppressive agent; IgE-mediated disorder;
 KW therapy; atopic allergy; anaphylactic hypersensitivity; asthma;
 KW allergic rhinitis; conjunctivitis; eczema; urticaria; food allergy;
 KW variable light chain; VL.
 XX
 OS Unidentified.
 XX
 XX US6723833-B1.
 XX
 PD 20-APR-2004.
 XX
 XX 17-NOV-2000; 2000US-00716028.
 PF
 XX 02-JUL-1997; 97US-0051554P.
 PR
 XX 02-JUL-1997; 97US-0051554P.
 PR

PR 30-JUN-1998; 98US-00109207.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Lowman HB, Presta LG, Jardieu PM, Lowe J;
 XX
 XX WPI; 2004-326922/30.
 DR
 XX New composition of an improved anti-IgE antibody or IgE binding fragment,
 PT useful for treating IgE-mediated diseases, e.g. atopic allergy, asthma,
 PT conjunctivitis, eczema, urticaria or food allergies.
 XX
 XX Claim 1; SEQ ID NO 15; 89pp; English.
 PS
 XX The invention relates to therapeutic compositions comprising anti-IgE
 CC antibody or IgE binding fragment in combination with an adjunct
 CC immunosuppressive agent. The composition is useful for treating IgE-
 CC mediated disorders. The disorders include atopic allergy associated with
 CC anaphylactic hypersensitivity and asthma, allergic rhinitis and
 CC conjunctivitis, eczema, urticaria and food allergies. The present
 CC sequence is an anti-IgE antibody variable light chain (VL).
 XX
 XX Sequence 218 AA;
 SQ

Query Match 100.0%; Score 596; DB 8; Length 218;
 Best Local Similarity 100.0%; Pred. No. 2.1e-35;
 Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DIQLTQSPSLASVGRVTITCRASKPVDGSDSYLNWYQQKPGKAPKLLIYAASYLE 60
 DB 1 DIQLTQSPSLASVGRVTITCRASKPVDGSDSYLNWYQQKPGKAPKLLIYAASYLE 60
 QY 61 GVPSRFGSGSGTDFLTITSSLPQEDPATYVCOQSHEDPYTFGGTKVEIKRTV 114
 DB 61 GVPSRFGSGSGTDFLTITSSLPQEDPATYVCOQSHEDPYTFGGTKVEIKRTV 114

RESULT 12
 ADN07038
 ID ADN07038 standard; protein; 218 AA.
 AC ADN07038;
 XX
 DT 01-JUL-2004 (first entry)
 DE Anti-IgE antibody e27 full length variable light chain (VL).
 XX
 KW Anti-IgE antibody; immunosuppressive agent; IgE-mediated disorder;
 KW therapy; atopic allergy; anaphylactic hypersensitivity; asthma;
 KW allergic rhinitis; conjunctivitis; eczema; urticaria; food allergy;
 KW variable light chain; VL.
 XX
 OS Unidentified.
 XX
 XX US6723833-B1.
 XX
 PD 20-APR-2004.
 XX
 XX 17-NOV-2000; 2000US-00716028.
 PF
 XX 02-JUL-1997; 97US-0051554P.
 PR 30-JUN-1998; 98US-00109207.
 XX
 XX (GETH) GENENTECH INC.
 PA
 XX Lowman HB, Presta LG, Jardieu PM, Lowe J;
 PI
 XX WPI; 2004-326922/30.
 DR
 XX New composition of an improved anti-IgE antibody or IgE binding fragment,
 PT useful for treating IgE-mediated diseases, e.g. atopic allergy, asthma,
 PT conjunctivitis, eczema, urticaria or food allergies.
 XX
 XX

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PS Claim 1; SEQ ID NO 17; 89pp; English.
XX
CC The invention relates to therapeutic compositions comprising anti-IgE
CC antibody or IgE binding fragment in combination with an adjunct
CC immunosuppressive agent. The composition is useful for treating IgE-
CC mediated disorders. The disorders include atopic allergy associated with
CC anaphylactic hypersensitivity and asthma, allergic rhinitis and
CC conjunctivitis, eczema, urticaria and food allergies. The present
CC sequence is an anti-IgE antibody variable light chain (VL).
XX
SQ Sequence 218 AA;

Query Match      100.0%; Score 596; DB 8; Length 218;
Best Local Similarity 100.0%; Pred. No. 2.1e-35;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLASVGDRTVITCRASKPVDGSDSYLNWYQKPKAPKLLIYAASYLE 60
DB 1 DIQLTQSPSSLASVGDRTVITCRASKPVDGSDSYLNWYQKPKAPKLLIYAASYLE 60
QY 61 GVPFRFSGSGGTDFTLTISLQPEDFATYYCQOSHEDPYTFGQGTKEIKRTV 114
DB 61 GVPFRFSGSGGTDFTLTISLQPEDFATYYCQOSHEDPYTFGQGTKEIKRTV 114

RESULT 13
ADN07040
ID ADN07040 standard; protein; 218 AA.
XX
AC ADN07040;
XX
DT 01-JUL-2004 (first entry)
XX
DE Anti-IgE antibody e26 and e27 variable light (VL) Fab fragment.
XX
KW Anti-IgE antibody; immunosuppressive agent; IgE-mediated disorder;
KW therapy; atopic allergy; anaphylactic hypersensitivity; asthma;
KW allergic rhinitis; conjunctivitis; eczema; urticaria; food allergy;
KW variable light chain; VL.
XX
OS Unidentified.
XX
XX US6723833-B1.
XX
PD 20-APR-2004.
XX
PF 17-NOV-2000; 2000US-00716028.
XX
PR 02-JUL-1997; 97US-0051554P.
PR 30-JUN-1998; 98US-00109207.
XX
PA (GETH ) GENENTECH INC.
XX
PI Lowman HB, Presta LG, Jardieu PM, Lowe J;
XX
XX WPI; 2004-326922/30.
XX
New composition of an improved anti-IgE antibody or IgE binding fragment,
PT useful for treating IgE-mediated diseases, e.g. atopic allergy, asthma,
PT conjunctivitis, eczema, urticaria or food allergies.
XX
PS Claim 7; SEQ ID NO 19; 89pp; English.
XX
CC The invention relates to therapeutic compositions comprising anti-IgE
CC antibody or IgE binding fragment in combination with an adjunct
CC immunosuppressive agent. The composition is useful for treating IgE-
CC mediated disorders. The disorders include atopic allergy associated with
CC anaphylactic hypersensitivity and asthma, allergic rhinitis and
CC conjunctivitis, eczema, urticaria and food allergies. The present
CC sequence is an anti-IgE antibody variable light chain (VL) Fab fragment.
XX
SQ Sequence 218 AA;

Query Match      100.0%; Score 596; DB 8; Length 218;
Best Local Similarity 100.0%; Pred. No. 2.1e-35;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLASVGDRTVITCRASKPVDGSDSYLNWYQKPKAPKLLIYAASYLE 60
DB 1 DIQLTQSPSSLASVGDRTVITCRASKPVDGSDSYLNWYQKPKAPKLLIYAASYLE 60
QY 61 GVPFRFSGSGGTDFTLTISLQPEDFATYYCQOSHEDPYTFGQGTKEIKRTV 114
DB 61 GVPFRFSGSGGTDFTLTISLQPEDFATYYCQOSHEDPYTFGQGTKEIKRTV 114

RESULT 14
AAW95653
ID AAW95653 standard; protein; 114 AA.
XX
AC AAW95653;
XX
DT 08-JUN-1999 (first entry)
XX
DE Mus musculus anti-IgE e26 & e27 variable light chain.
XX
KW Variable light chain; IgE; antibody; anti-IgE; reduction; prevention;
KW histamine; production; hypersensitivity; allergen; anaphylaxis;
KW atopic allergy; asthma; allergic rhinitis; conjunctivitis; hay fever;
KW eczema; anaphylactic shock; urticaria.
XX
OS Mus musculus.
XX
XX WO9901556-A2.
XX
PD 14-JAN-1999.
XX
PF 30-JUN-1998; 98WO-US013410.
XX
PR 02-JUL-1997; 97US-00887352.
XX
PA (GETH ) GENENTECH INC.
XX
PI Lowman HB, Presta LG, Jardieu PM, Lowe J;
XX
XX WPI; 1999-106057/09.
XX
Improving affinity of polypeptides, particularly anti-IgE antibodies - by
PT identifying aspartyl residues which undergo isomerisation and
PT substituting alternative residues and screening for affinity against the
PT target.
XX
PS Disclosure; Page 89; 129pp; English.
XX
XX The sequence is that of the variable light chain of e26 and e27. It was
XX used as part of a method to improve the affinity of anti-IgE antibodies
XX such as e26 and e27. The e26 and e27 antibodies can be used for reducing
XX or preventing IgE mediated production of histamine in a mammal. They can
XX be used for treating a disorder mediated by IgE such as hypersensitivity,
XX atopic allergy, asthma, allergic rhinitis, conjunctivitis, hay fever,
XX eczema, anaphylactic shock and urticaria. The antibodies can also be used
XX for affinity purification, detection and diagnosis
XX
SQ Sequence 114 AA;

Query Match      99.7%; Score 594; DB 2; Length 114;
Best Local Similarity 99.1%; Pred. No. 1.6e-35;
Matches 113; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIQLTQSPSSLASVGDRTVITCRASKPVDGSDSYLNWYQKPKAPKLLIYAASYLE 60
DB 1 DIQLTQSPSSLASVGDRTVITCRASKPVDGSDSYLNWYQKPKAPKLLIYAASYLE 60
QY 61 GVPFRFSGSGGTDFTLTISLQPEDFATYYCQOSHEDPYTFGQGTKEIKRTV 114
DB 61 GVPFRFSGSGGTDFTLTISLQPEDFATYYCQOSHEDPYTFGQGTKEIKRTV 114

```

Search completed: June 3, 2005, 09:09:07
Job time : 38.3502 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 3, 2005, 08:53:28 ; Search time 7.09576 Seconds
(without alignments)
1545.812 Million cell updates/sec

Title: US-10-791-619-11

Perfect score: 623

Sequence: 1 EVQLVESGGGLVQPGGSLRL.....YCARSHYFGHWFAVWGQG 114

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	419	67.3	140	2 S31588	Ig heavy chain V r
2	418.5	67.2	140	2 S70442	Ig heavy chain pre
3	418	67.1	123	2 S31114	Ig heavy chain - h
4	416	66.8	138	2 S31666	Ig heavy chain V r
5	413	66.3	121	2 S31113	Ig heavy chain - h
6	411.5	66.1	147	2 S31780	Ig variable region
7	409.5	65.7	122	2 S36005	Ig heavy chain V r
8	409.5	65.7	128	2 S48797	Ig heavy chain V r
9	409.5	65.7	141	2 S31669	Ig heavy chain V r
10	408	65.5	125	2 S30531	Ig heavy chain V r
11	407	65.3	117	2 S36259	Ig heavy chain V r
12	407	65.3	119	2 S31107	Ig heavy chain - h
13	404.5	64.9	122	2 S31117	Ig heavy chain - h
14	404	64.8	121	2 S31966	Ig heavy chain V r
15	404	64.8	121	2 S36005	Ig heavy chain V r
16	404	64.8	135	2 S31598	Ig heavy chain V r
17	404	64.8	140	2 S31686	Ig heavy chain V r
18	403	64.7	137	2 S38489	Ig heavy chain V r
19	401.5	64.4	127	2 S31701	Ig heavy chain - h
20	401	64.4	123	2 S26794	Ig heavy chain V r
21	400.5	64.3	124	2 S20782	Ig heavy chain V r
22	399.5	64.1	114	2 S36280	Ig heavy chain V r
23	399.5	64.1	136	2 S31587	Ig heavy chain V r
24	399	64.0	119	2 S31108	Ig heavy chain - h
25	399	64.0	160	2 S05271	Ig heavy chain pre
26	398	63.9	119	2 S36005	Ig heavy chain V r
27	398	63.9	143	2 S23624	Ig heavy chain V r
28	397	63.7	132	2 S31603	Ig heavy chain V r
29	396.5	63.6	116	2 S31110	Ig heavy chain - h

30	396	63.6	120	1 M3HUBW	Ig heavy chain V-I
31	396	63.6	130	2 S31601	Ig heavy chain V r
32	396	63.6	139	2 S37781	Ig variable region
33	395.5	63.5	118	2 S31116	Ig heavy chain - h
34	395.5	63.5	120	2 S48798	Ig heavy chain V r
35	395.5	63.5	139	2 S31674	Ig heavy chain V r
36	395	63.4	119	2 S36005	Ig heavy chain V r
37	395	63.4	121	2 S56773	Ig heavy chain - h
38	395	63.4	134	2 S31699	Ig heavy chain V r
39	394.5	63.3	114	2 S46390	Ig heavy chain V r
40	394.5	63.3	122	2 PC2398	anti-tetanus toxin
41	394	63.2	119	2 F36005	Ig heavy chain V r
42	394	63.2	134	2 S31679	Ig heavy chain V r
43	393.5	63.2	122	1 M3HUM	Ig heavy chain V-I
44	393.5	63.2	128	2 S26790	Ig heavy chain V r
45	393	63.1	117	2 S78486	Ig heavy chain V r

ALIGNMENTS

RESULT 1

S31588

Ig heavy chain V region - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C:Accession: S31588

R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelles, C.

submitted to the EMBL Data Library, June 1992

A:Description: Mechanisms that generate human immunoglobulin diversity operate from the

A:Reference number: S31585

A:Accession: S31588

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-140 <CUI>

A:Cross-references: EMBL:Z14200; NID:G30957; PIDN:CAA78569.1; PID:G30958

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 67.3%; Score 419; DB 2; Length 140;

Best Local Similarity 71.3%; Pred. No. 2.5e-30;

Matches 82; Conservative 12; Mismatches 19; Indels 2; Gaps 2;

QY 1 EVQLVESGGGLVQPGGSLRLSCAASGFTSS-AMSVWRQAPGKLEWVASIKYS-GETK 59

Db 20 EVQLVESGGGLVQPGGSLRLSCAASGFTSS-AMSVWRQAPGKLEWVASIKYS-GETK 78

QY 60 YNPVKGRITISRDSDKNTFYLQMSLRAEDTAVYICARSHYFGHWFAVWGQG 114

Db 79 YADSVKGRFTISRDSDKNTFYLQMSLRAEDTAVYICARSHYFGHWFAVWGQG 133

RESULT 2

S70442

Ig heavy chain precursor V region (mu) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004

C:Accession: S70442

R:Cuisinier, A.M.; Fumoux, F.; Fougereau, M.; Tonnelles, C.

Mol. Immunol. 29, 1363-1373, 1992

A:Title: IGM kappa/lambda EBV human B cell clone: an early step of differentiation of fet

A:Reference number: S70442; MUID:93024508; PMID:1383695

A:Accession: S70442

A>Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-140 <CUI>

A:Cross-references: UNIPROT:Q8WUK1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 67.2%; Score 418.5; DB 2; Length 140;

Best Local Similarity 72.2%; Pred. No. 2.7e-30;

Db 79 YADSVKGRFTISRDNKNTLYLQNSLRAEDTAVYYCAKAR--TGYWYFDLWGRG 131

RESULT 5

S31113

IG heavy chain - human

C/Species: Homo sapiens (man)

C/Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999

C/Accession: S31113

R/Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman, Eur. J. Immunol. 22, 247-251, 1992

A/Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complement A;Reference number: S31104; MUID:92111633; PMID:1730252

A/Accession: S31113

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: mRNA

A/Residues: 1-121 <PAA>

A/Cross-references: EMBL:X62962

A/Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 66.3%; Score 413; DB 2; Length 121;

Best Local Similarity 70.4%; Pred. No. 7.2e-30;

Matches 81; Conservative 13; Mismatches 19; Indels 2; Gaps 2;

Qy 1 EVLVESGGGLVQPGGSLRLSCA VSGYITSGYSNNWIRQAPKGLEWVASIKYS-GETK 59

Db 1 EVLVESGGGLVQPGGSLRLSCA SGFTFS-YAMSWVRQAPKGLEWVASISGSGSTY 59

Qy 60 YNPVSKGRITISRDDSKNTFLQNSLRAEDTAVYYCARGSHYFGHHFPAVMQGG 114

Db 60 YADSVKGRFTISRDNKNTLYLQNSLRAEDTAVYYCATDWMGPFYGRSAFDIMQGG 114

RESULT 6

I37780

IG variable region (VDJ) (clone T20-11) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 23-Jul-1999

C/Accession: I37780; S25474

R/Demailson, C.; Chastagner, P.; Theze, J.; Zouali, M. Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994

A/Title: Somatic diversification in the heavy chain variable region genes expressed by h A;Reference number: A36876; MUID:94119917; PMID:8290556

A/Accession: I37780

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-147 <RES>

A/Cross-references: EMBL:X67943; NID:G33578; PIDN:CAA48130.1; PID:G33579

C/Superfamily: immunoglobulin V region; immunoglobulin homology

F;28-111/Domain: immunoglobulin homology <IMM>

Query Match 66.1%; Score 411.5; DB 2; Length 147;

Best Local Similarity 70.3%; Pred. No. 1.2e-29;

Matches 83; Conservative 12; Mismatches 18; Indels 5; Gaps 3;

Qy 1 EVLVESGGGLVQPGGSLRLSCA VSGYITSGYSNNWIRQAPKGLEWVASIKYSGETK- 59

Db 14 EVLVESGGGLVQPGGSLRLSCA SGFTFS-YNMSWVRQAPKGLEWVANIKDQSEK 72

Qy 60 YNPVSKGRITISRDDSKNTFLQNSLRAEDTAVYYCARGSHYFGHHWF---AVWGQG 114

Db 73 YADSVKGRFTISRDNKNTLYLQNSLRAEDTAVYYCAKDGEGWGLYYYYYGMVWGQG 130

RESULT 7

E36005

IG heavy chain V region (M72) - human

C/Species: Homo sapiens (man)

C/Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998

C/Accession: E36005


```

R:Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A:Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A:Reference number: A36005; MUID:90349571; PMID:2117273
A:Accession: E36005
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-122 <SCH>
A:Cross-references: GB:M34030
C:Genetics:
A:Gene: GDB:IGH@; IGH@Y1
A:Cross-references: GDB:118731; OMTM:146910
A:Map position: 14q32.33-14q32.33
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match      65.7%; Score 409.5; DB 2; Length 122;
Best Local Similarity 70.1%; Pred. No. 1.5e-29;
Matches 82; Conservative 11; Mismatches 19; Indels 5; Gaps 4;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNNWIRQAPGKLEWVASIKYSGTK- 59
Db 1 QVQLVESGGGVQPGGSLRLSCAASGFTFSS-YAMHWVRQAPGKLEWVAIVSYDGSNKY 59
Qy 60 YNPVSKGRITTSRDDSKNTFYLNQSLRAEDTAVYICARGSHYFGHWHFA--VWGQ 114
Db 60 YADSVKGRFTISRDNKNTLYLNQSLRAEDTAVYICARDRH--SSWYIGMDVWGQ 115

RESULT 8
S48797
Ig heavy chain V region (anti-Sm, VH3/Dxp4/JH6) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Sep-1998 #text_change 23-Jul-1999
C:Accession: S48797; S26893
R:Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
submitted to the EMBL Data Library, October 1994
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of
A:Description: Molecular characterization of natural human anti-Sm autoantibodies.
A:Reference number: S48797
A:Accession: S48797
A:Molecule type: mRNA
A:Residues: 1-128 <MAH>
A:Cross-references: EMBL:Z46379; NID:G587147; PIDN:CAA86512.1; PID:gl340168
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of
A:Reference number: S26885; MUID:93021117; PMID:1404388
A:Accession: S26893
A:Molecule type: DNA
A:Residues: 1-98 <TOM>
A:Cross-references: EMBL:Z12350; NID:G32922; PIDN:CAA78220.1; PID:G32923
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match      65.7%; Score 409.5; DB 2; Length 128;
Best Local Similarity 67.2%; Pred. No. 1.6e-29;
Matches 82; Conservative 15; Mismatches 16; Indels 9; Gaps 4;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNNWIRQAPGKLEWVASIKYSGTK- 59
Db 1 QVQLVESGGGVQPGGSLRLSCAASGFTFSS-YGMHWVRQAPGKLEWVAIVYDGSNKY 59
Qy 60 YNPVSKGRITTSRDDSKNTFYLNQSLRAEDTAVYICARGSHYF---GHWHF---AVWG 112
Db 60 YADSVKGRFTISRDNKNTLYLNQSLRAEDTAVYICARDNTYDSSGYYTYGMDVWG 119
Qy 113 QG 114
Db 120 QG 121
```

```

RESULT 9
S31669
Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31669
R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.
submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
A:Reference number: S31585
A:Accession: S31669
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-141 <CUI>
A:Cross-references: EMBL:Z14212; NID:G30959; PIDN:CAA78581.1; PID:G30960
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match      65.7%; Score 409.5; DB 2; Length 141;
Best Local Similarity 70.7%; Pred. No. 1.7e-29;
Matches 82; Conservative 12; Mismatches 19; Indels 3; Gaps 3;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNNWIRQAPGKLEWVASIKYSGE-TK 59
Db 20 EVQLVESGGGLVQPGGSLRLSCAASGFTFSS-YSNWVRQAPGKLEWVSSISSSSYIY 78
Qy 60 YNPVSKGRITTSRDDSKNTFYLNQSLRAEDTAVYICARGSHYFGH-WHFAVWGQ 114
Db 79 YADSVKGRFTISRDNKNTLYLNQSLRAEDTAVYICARGHRLTGEKGYFDLWGRG 134

RESULT 10
S30531
Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: S30531
R:Mariette, X.
submitted to the EMBL Data Library, October 1992
A:Reference number: S30520
A:Accession: S30531
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-125 <MAR>
A:Cross-references: UNIPROT:Q9UJ91; EMBL:Z18317
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match      65.5%; Score 408; DB 2; Length 125;
Best Local Similarity 69.2%; Pred. No. 2.1e-29;
Matches 83; Conservative 11; Mismatches 18; Indels 8; Gaps 4;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNNWIRQAPGKLEWVASIKYGET-K 59
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSS-YSNWVRQAPGKLEWISYISSSSSTIY 59
Qy 60 YNPVSKGRITTSRDDSKNTFYLNQSLRAEDTAVYICAR-----GSHYFGHWHFAVWGQ 114
Db 60 YADSVKGRFTISRDNKNTLYLNQSLRAEDTAVYICARSRNYDSSGYSH-YFDYWGQ 118

RESULT 11
S36259
Ig heavy chain V region (clone alpha-TNF-A1) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C:Accession: S36259
R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.;
EMBO J. 12, 725-734, 1993
A:Title: Human anti-self antibodies with high specificity from phage display libraries.
A:Reference number: S36256; MUID:93178448; PMID:7679990
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Search completed: June 3, 2005, 09:17:50
Job time : 7.09576 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 3, 2005, 08:31:37 ; Search time 32.7497 Seconds
(without alignments)
1782.523 Million cell updates/sec

Title: US-10-791-619-11

Perfect score: 623

Sequence: 1 EVQLVSGGGLVQFGSSRL.....YCARSHYFGHHFAVWQG 114

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	413	66.3	470	2	Q6PJA4	Q6pia4 homo sapien
2	408	65.5	113	2	Q9UL90	Q9ul90 homo sapien
3	399	64.0	466	2	Q6IN78	Q6in78 homo sapien
4	398	63.9	478	2	Q6PI81	Q6pi81 homo sapien
5	397.5	63.8	118	2	Q9UL72	Q9ul72 homo sapien
6	396	63.6	120	1	HV3E_HUMAN	P01766 homo sapien
7	394.5	63.3	613	2	Q8WUK1	Q8wuk1 homo sapien
8	394	63.2	240	2	Q6SZC9	Q6szc9 homo sapien
9	394	63.2	472	2	Q6N089	Q6n089 homo sapien
10	393.5	63.2	122	1	HV3G_HUMAN	P01768 homo sapien
11	392.5	63.0	118	2	Q9UL91	Q9ul91 homo sapien
12	391.5	62.8	473	2	Q6MZV7	Q6mzv7 homo sapien
13	391.5	62.8	606	2	Q6GMV2	Q6gmv2 homo sapien
14	391	62.8	597	2	Q96BB9	Q96bb9 homo sapien
15	389.5	62.5	475	2	Q6MZQ6	Q6mzq6 homo sapien
16	389	62.4	116	2	Q9UL93	Q9ul93 homo sapien
17	389	62.4	121	2	Q9UL71	Q9ul71 homo sapien
18	389	62.4	464	2	Q6MZU6	Q6mzu6 homo sapien
19	385	61.8	123	1	HV24_MOUSE	P01793 mus musculus
20	384.5	61.7	116	1	HV05_CARAU	P19181 carassius a
21	383.5	61.6	573	2	Q8WU38	Q8wu38 homo sapien
22	382.5	61.4	147	2	Q9Y509	Q9y509 homo sapien
23	382	61.3	117	1	HV3C_HUMAN	P01764 homo sapien
24	381	61.2	493	2	Q6GMX2	Q6gmux2 homo sapien
25	380.5	61.1	494	2	Q9EK68	Q9ek68 homo sapien
26	377.5	60.6	112	2	Q9HCC1	Q9hcc1 homo sapien
27	377	60.5	493	2	Q8NCL6	Q8ncl6 homo sapien
28	374	60.0	115	1	HV3F_HUMAN	P01767 homo sapien
29	374	60.0	123	1	HV22_MOUSE	P01791 mus musculus
30	374	60.0	499	2	Q8N5K4	Q8n5k4 homo sapien
31	372	59.7	119	1	HV31_HUMAN	P01770 homo sapien

32	371	59.6	487	2	Q80Z17	Q80z17 mus musculus
33	370	59.4	121	1	HV3J_HUMAN	P01771 homo sapien
34	369.5	59.3	122	1	HV20_MOUSE	P01789 mus musculus
35	368.5	59.1	479	2	Q6MZV6	Q6mzv6 homo sapien
36	368.5	59.1	487	2	Q6ZVX0	Q6zvxo homo sapien
37	367	58.9	470	2	Q7Z5W1	P01751 homo sapien
38	366.5	58.8	114	1	HV3B_HUMAN	P01763 homo sapien
39	366.5	58.8	122	1	HV21_MOUSE	P01790 mus musculus
40	366.5	58.8	487	2	Q9KX44	Q9kxa4 mus musculus
41	365	58.6	123	1	HV18_MOUSE	P01787 mus musculus
42	365	58.6	123	1	HV23_MOUSE	P01792 mus musculus
43	364	58.4	123	1	HV19_MOUSE	P01788 mus musculus
44	364	58.4	137	1	HV46_MOUSE	P01822 mus musculus
45	363	58.3	113	1	HV30_MOUSE	P01799 mus musculus

ALIGNMENTS

RESULT 1
Q6PJA4 PRELIMINARY; PRT; 470 AA.
AC Q6PJA4;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalios D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
ET and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX Strausberg R.;
RA Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018747; AAH18747.1; -.
DR HSSP; P01861; IADO.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.

RX MEDLINE=22388257; PubMed=12472932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Wozny K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyzanski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
SEQUENCE FROM N.A.
RP TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC041037; AAH41037.1; -;
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG c1.
DR InterPro; IPR003006; IG-MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; CI-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG MHC; UNKNOWN 2.
KW Hypothetical protein.
SQ SEQUENCE 478 AA; 17BED38D91970D6 CRC64;
Query Match 63.9%; Score 398; DB 2; Length 478;
Best Local Similarity 65.3%; Pred. No. 4.2e-32;
Matches 81; Conservative 15; Mismatches 16; Indels 12; Gaps 4;
OY 1 EVQLVESGGGLVQPGGSLRLSCA VSGYSITSGYSNNWIRQAPGKLEWVSIKYSGETKY 60
DB 20 EVQLVESGGGLVQPGGSLRLSCA ASGFTFS-YNMSWVRQAPGKLEWVNIKQDSEKY 78
OY 61 N-PSVKGRITISRDNSKNTFYLMNSLRADTA VYTCAR-----GSHYFGHHFPAV 110
DB 79 YVDSVKGRFTISRDNKNSLYLMNSLRADTA VYTCAREFESTTNTVNDYY-YFYMDV 137
OY 111 WQOG 114
DB 138 WKGK 141
RESULT 5
Q9UL72 PRELIMINARY; PRT; 118 AA.
AC Q9UL72;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE=98271739; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Werwe F.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL; AF035042; AAD56278.1; -;
DR PIR; S21205; S21205.
DR HSSP; P01783; IIGC.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 118
FT NON_TER 118
SQ SEQUENCE 118 AA; 12872 MW; B4D1A5944B2D5CCA CRC64;
Query Match 63.8%; Score 397.5; DB 2; Length 118;
Best Local Similarity 72.2%; Pred. No. 1e-32;
Matches 83; Conservative 9; Mismatches 18; Indels 5; Gaps 4;
OY 1 EVQLVESGGGLVQPGGSLRLSCA VSGYSITSGYSNNWIRQAPGKLEWVSIKYS-GETK 59
DB 1 EVQLVESGGGLVQPGGSLRLSCA ASGFTVSSNY-MNWSVRQAPGKLESV-SVTYSGSSY 58
OY 60 YNPSVKGRITISRDNSKNTFYLMNSLRADTA VYTCARGSHYFGHHFPAVWQOG 114
DB 59 YADSVKGRFTISRDNKNTLYLMNSLRADTA VYTCARDR--FGELFDYWGOG 111
RESULT 6
HV3E_HUMAN STANDARD; PRT; 120 AA.
ID HV3E_HUMAN
AC P01766;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig heavy chain V-III region BRO.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=71117674; PubMed=65324; DOI=10.1016/0019-2791(76)90271-8;
RA Capra J.D., Hopper J.E.;
RT "Comparative studies on monotypic IGM lambda and Igg kappa from an
RT individual patient. III. The complete amino acid sequence of the VH
RT region of the IGM paraprotein";
RL Immunochimistry 13:995-999 (1976).
CC -!- MISCELLANEOUS: This chain was obtained from IGM isolated from the
CC serum of a patient with malignant lymphoma of the Waldenstrom
CC type.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02049; M3HUEW.
DR HSSP; P01783; IIGC.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 111 Ig-like.
FT NON_TER 120
FT NON_TER 120
SQ SEQUENCE 120 AA; 13227 MW; D3F0428F7C2E6410 CRC64;
Query Match 63.6%; Score 396; DB 1; Length 120;
Best Local Similarity 65.0%; Pred. No. 1.5e-32;
Matches 80; Conservative 12; Mismatches 17; Indels 14; Gaps 3;

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SQ  SEQUENCE  613 AA,  67295 MW,  60C7F5950671E315 CRC64;

Query Match      63.3%; Score 394.5; DB 2; Length 613;
Best Local Similarity 66.7%; Pred. No. 1.3e-31;
Matches 80; Conservative 10; Mismatches 17; Indels 13; Gaps 4;

QY  1  EVLVESGGGLVOPGSLRLSCAVGYSYTSYGSMWIRQAPQKGLEWVASIKYGETK- 59
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  20  QVQLVSGGSGVQPGKSLRLSCAASGFTFS- YGMEHWVRQAPQKGLEWVAIVSDGSNKY 78
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY  60  YNPVVKGRITIRDRDSKNTFYLOMNSLRADETAVYYCARGSHYFGHH-----FAVWGQG 114
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db  79  YADVVKGRFTIRSDNSKNTLYLOMNSLRADETAVYYCAK-----DWSEGEVETDIWGQG 132
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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RESULT 8
Q65ZC9 PRELIMINARY; PRT; 240 AA.
ID AC Q65ZC9;
DT 25-OCT-2004 (TREMblrel. 28, Created)
DT 25-OCT-2004 (TREMblrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMblrel. 28, Last annotation update)
DE Single-chain Fv (Fragment).
GN Name=scFv;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C1q/7;
RX MEDLINE=97362799; PubMed=9219263;
RA Kontermann R.E., Wing M.G.; Winter G.;
RT "Complement recruitment using bispecific diabodies.";
RL Nat. Biotechnol. 15:629-631(1997).
DR EMBL; Y13056; CAA73499.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
FT NON_TER 1
FT NON_TER 240
FT NON_TER 240
SQ SEQUENCE 240 AA; 25569 MW; FDCFD3645P64B373 CRC64;

Query Match 63.2%; Score 394; DB 2; Length 240;
Best Local Similarity 68.4%; Pred. No. 5e-32;
Matches 80; Conservative 11; Mismatches 16; Gaps 4;

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Qy	1	EVLVTSGGGLVPQGSGSLRLSCAVSGSYSTGYSWNWIRQAQPGKGLEWVASIKYSGETK-	59
Dd	1	QVLVTSGGGLVPQGSGSLRLSCAAAGTFFSS-YGMHWVRQAQPGKLEWVAIVSYDGSNKY	59
Qy	60	YNPSVKGRTTISRDDSKNTFYLQMNSLRRAEDTAVYYCARGSHYFGWHHPAV--WGQG	114
Dd	60	YADSVKGRFTISRDKNSKNTFYLMNLSRRAEDTAVYYCAR-----DWGSDLPWKKG	110
 RESULT 9 Q6N089 PRELIMINARY; PRT; 472 AA. 			
ID	Q6N089		
AC	Q6N089;		
DT	05-JUL-2004	(TrEMBLrel. 27, Created)	
DT	05-JUL-2004	(TrEMBLrel. 27, Last sequence update)	
DT	05-JUL-2004	(TrEMBLrel. 27, Last annotation update)	
DE	Hypothetical protein DKFZp686P15220.		
GN	Name=DKFZp686P15220;		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI TaxID=9606;		


```
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Anid C., Osanger A.,
RG Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640627; CAB45781.1; -
DR HSSP; P01861; 1ADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; CI-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS08335; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;

Query Match 63.2%; Score 394; DB 2; Length 472;
Best Local Similarity 66.7%; Pred. No. 1.1e-31;
Matches 78; Conservative 14; Mismatches 21; Indels 4; Gaps 3;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSNNWIRQAPGKGLEWVASIKY-SGETK 59
Db 20 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSNNWIRQAPGKGLEWVSGISWNSG 78
Qy 60 YNPVSKGRITISRDTSKNTFYLQNSLRADTAVYTCAR--GSHYFGHHFAVWGQ 114
Db 79 YADSVKGRFTISRDNKNSLYLQNSLRADTAVYCAKEIQAHHFYFGYMDVWGQ 135

RESULT 10
HV3G_HUMAN STANDARD; PRT; 122 AA.
AC P01768;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig heavy chain V-III region CMM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=81013859; PubMed=6774332;
RA Lehman D.W., Putnam F.W.;
RT "Amino acid sequence of the variable region of a human mu chain: location of a possible JH segment.";
RT Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).
CC -!- MISCELLANEOUS: This mu chain was isolated from the plasma of a patient with macroglobulinemia.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR HSSP; P01772; 2F8A.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS08335; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region;
KW Pyroliadone carboxylic acid.
DOMAIN 1 112 Ig-like.
FT MOD_RES 1 1 Pyroliadone carboxylic acid.
FT NON_TER 122
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SQ SEQUENCE 122 AA; 13668 MW; A42D0F17D252F1C2 CRC64;

Query Match 63.2%; Score 393.5; DB 1; Length 122;
Best Local Similarity 65.5%; Pred. No. 2.7e-32;
Matches 76; Conservative 15; Mismatches 22; Indels 3; Gaps 3;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSNNWIRQAPGKGLEWVASIKYSGETKY 60
Db 1 QVELVESGGGVVZPGRSLRLSCAASGFTF--SNYAMHWVRQPGKGLEWVAIVSYGBBKY 59
Qy 61 NP-SVKGRITISRDTSKNTFYLQNSLRADTAVYTCARGSHYFGHHF-FAVWGQ 114
Db 60 YADSVKGRFTISRDBSKNTELYLQNSLRADTAVYTCARDRLYGYRAFNWVGQ 115

RESULT 11
Q9UL91 PRELIMINARY; PRT; 118 AA.
AC Q9UL91;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus.";
RT Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035023; AAD56259.1; -
DR PIR; PH0875; PH0875.
DR PIR; S21205; S21205.
DR PIR; S30531; S30531.
DR HSSP; P01783; 1IGC.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS08335; IG LIKE; 1.
FT NON_TER 118
FT NON_TER 118
SQ SEQUENCE 118 AA; 12843 MW; D0633949F2AC149D CRC64;

Query Match 63.0%; Score 392.5; DB 2; Length 118;
Best Local Similarity 70.4%; Pred. No. 3.3e-32;
Matches 81; Conservative 10; Mismatches 19; Indels 5; Gaps 3;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSNNWIRQAPGKGLEWVASIKYSGE-K 59
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSS--YSNNWVRQAPGKGLEWVSYISITITLY 59
Qy 60 YNPVSKGRITISRDTSKNTFYLQNSLRADTAVYTCARGSHYFGHHFAVWGQ 114
Db 60 YADSVKGRFTISRDNKNSLYLQNSLRADTAVYTCARGD---SSEAFDIWGQ 111

RESULT 12
Q6MZV7 PRELIMINARY; PRT; 473 AA.
AC Q6MZV7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFP686C11235.
GN Name=DKFP686C11235;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human small intestine;
RG The German Human cDNA Consortium;
RA Bloecker H., Boecker M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
RM EMBL; BX640853; CAB45920.1; -.
DR HSP; P01863; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 52121 MW; 94762AE4C0BFC447 CRC64;

Query Match 62.8%; Score 391.5; DB 2; Length 473;
Best Local Similarity 64.4%; Pred. No. 1.9e-31;
Matches 76; Conservative 17; Mismatches 20; Indels 5; Gaps 3;

QY 1 EVQLVGGGLVQPGGSLRLSCAAGTSSGYSITSGYSNWIRQAPGKLEWVASIKYSGET-K 59
DB 20 EIQLVGGGLVQPGGSLRLSCAAGTSSGYSITSGYSNWIRQAPGKLEWVASIKYSGET-K 59
QY 60 YNPSVKGRITISRDSDKNTFYLQNSLRADETAVYYCARGSHYFGHW---FAVWGQ 114
DB 79 YADSLQGRFTISRDNARNSLYQNSLRADETAVYYCARGNEHTSPYFPFFDYGQ 136

RESULT 13
Q6GM2 ID Q6GM2 PRELIMINARY; PRT; 606 AA.
AC Q6GM2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RM MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyzanski M.I., Skalska U., Smallos D.B., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
```

```
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RM EMBL; BC073758; AAH73758.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 606 AA; 66184 MW; B6B38B5114E4C55 CRC64;

Query Match 62.8%; Score 391.5; DB 2; Length 606;
Best Local Similarity 62.5%; Pred. No. 2.5e-31;
Matches 80; Conservative 13; Mismatches 20; Indels 15; Gaps 3;

QY 1 EVQLVGGGLVQPGGSLRLSCAAGTSSGYSITSGYSNWIRQAPGKLEWVASIKYSGE-TK 59
DB 20 QVQLVGGGLVQPGGSLRLSCAAGTFTFSDYMSWIRQAPGKLEWVSISSSSVTN 78
QY 60 YNPSVKGRITISRDSDKNTFYLQNSLRADETAVYYCARGSH-----YFGHW 106
DB 79 YADSVKGRFTISRDNAKNSLYQNSLRADETAVYYCARGNGIAAGRVVYAEYVVY 138

QY 107 HFAVWGQ 114
DB 139 GMDVWGQ 146

RESULT 14
Q96BB9 ID Q96BB9 PRELIMINARY; PRT; 597 AA.
AC Q96BB9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RM MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyzanski M.I., Skalska U., Smallos D.B., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
```


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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 3, 2005, 08:53:28 ; Search time 7.09576 seconds
(without alignments)
1545.812 Million cell updates/sec

Title: US-10-791-619-12

Perfect score: 625

Sequence: 1 EVQLVESGGGLVQPGSLRL.....YCARGSHYFGHWHPAVWGQG 114

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Pir1.*
2: Pir2.*
3: Pir3.*
4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	420.5	67.3	140	2 S70442	Ig heavy chain pre
2	420	67.2	140	2 S31588	Ig heavy chain v r
3	419	67.0	123	2 S31114	Ig heavy chain - h
4	417	66.7	138	2 S31666	Ig heavy chain v r
5	415.5	66.5	122	2 E36005	Ig heavy chain v r
6	415.5	66.5	128	2 S48797	Ig heavy chain v r
7	414	66.2	121	2 S31117	Ig heavy chain - h
8	410.5	65.7	141	2 S31669	Ig heavy chain - h
9	410.5	65.7	141	2 S31117	Ig heavy chain v r
10	410.5	65.7	147	2 S31780	Ig variable region
11	410	65.6	121	2 S19666	Ig heavy chain v r
12	410	65.6	121	2 G36005	Ig heavy chain v r
13	409	65.4	117	2 S36259	Ig heavy chain v r
14	409	65.4	125	2 S30531	Ig heavy chain v r
15	408	65.3	119	2 S31107	Ig heavy chain - h
16	407.5	65.2	137	2 S31701	Ig heavy chain v r
17	406	65.0	135	2 S31598	Ig heavy chain v r
18	405	64.8	140	2 S31686	Ig heavy chain v r
19	404	64.6	127	2 S38489	Ig heavy chain - h
20	403	64.5	132	2 S31603	Ig heavy chain v r
21	402	64.3	123	2 S26794	Ig heavy chain v r
22	402	64.3	130	2 S31601	Ig heavy chain v r
23	401.5	64.2	138	2 S31116	Ig heavy chain - h
24	401.5	64.2	139	2 S31674	Ig heavy chain v r
25	400.5	64.1	114	2 S46390	Ig heavy chain v r
26	400	64.0	119	2 S31108	Ig heavy chain - h
27	400	64.0	119	2 F36005	Ig heavy chain v r
28	400	64.0	134	2 S31679	Ig heavy chain v r
29	400	64.0	160	2 S05271	Ig heavy chain pre

30	399.5	63.9	116	2 S31110	Ig heavy chain - h
31	399.5	63.9	124	2 S20782	Ig heavy chain v r
32	399	63.8	119	2 D36005	Ig heavy chain v r
33	399	63.8	130	2 PLO098	Ig heavy chain pre
34	399	63.8	143	2 S23624	Ig heavy chain v r
35	398.5	63.8	114	2 S36280	Ig heavy chain v r
36	398.5	63.8	136	2 S31587	Ig heavy chain v r
37	397.5	63.6	122	2 PC2398	anti-tetanus toxin
38	397	63.5	117	2 S36270	Ig heavy chain v r
39	396.5	63.4	120	2 S48798	Ig heavy chain v r
40	396	63.4	119	2 C36005	Ig heavy chain v r
41	396	63.4	121	2 I55673	Ig heavy chain - h
42	396	63.4	121	2 S31104	Ig heavy chain (su
43	396	63.4	134	2 S31699	Ig heavy chain v r
44	395.5	63.3	114	2 S46391	Ig heavy chain v r
45	395	63.2	123	2 S38493	Ig heavy chain - h

ALIGNMENTS

RESULT 1

S70442
Ig heavy chain precursor V region (mu) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C:Accession: S70442
R:Cuisinier, A.M.; Fumoux, F.; Fougereau, M.; Tonnelles, C.
Mol. Immunol. 29, 1363-1373, 1992
A:Title: IGM kappa/lambda EBV human B cell clone: an early step of differentiation of fet
A:Reference number: S70442; MUID:93024508; PMID:1383695
A:Accession: S70442
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-140 <CUI>
A:Cross-references: UNIPROT:Q8WUK1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match		67.3%	Score 420.5; DB 2; Length 140;
Best Local Similarity		73.0%;	Pred. No. 6.1e-30;
Matches		84; Conservative	8; Mismatches 20; Indels 3; Gaps 3;
Qy	1	EVQLVESGGGLVQPGSLRLSCA	VSIGSYISITSGYSNNWIRQAPGKLEWVASTYDGSTN- 59
Db	20	QVQLVESGGGVQPGSLRLSCA	ASGFTF-SNYGMHWVRQAPGKLEWVAFIRYDGSNKY 78
Qy	60	YNPSVKGRITISRDDSKNTFY	LQMSLRADTAVYVCARGSHYFGHWHPAVWGQG 114
Db	79	YADSVKGRFTISRDNKNTLY	LQMSLRADTAVYVCAR-DHIVGATFYDYGQG 132

RESULT 2

S31588
Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31588
R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelles, C.
submitted to the EMBL Data Library June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
A:Reference number: S31588
A:Accession: S31588
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-140 <CUI>
A:Cross-references: EMBL:Z14200; NID:g30957; PIDN:CAA78569.1; PID:g30958
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 67.2%; Score 420; DB 2; Length 140;
Best Local Similarity 71.3%; Pred. No. 6.7e-30;

Db 79 YADSVKGRFTISRDNKNTLYLQWNSLRADTAVYYCAKAR--TGTYWFDLWGRR 131

RESULT 5
E36005
Ig heavy chain V region (M72) - human
C/Species: Homo sapiens (man)
C/Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998
C/Accession: E36005
R/Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A/Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene A/reference number: A36005; MUID:90349571; PMID:2117273
A/Accession: E36005
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-122 <SCH>
A/Cross-references: GB:M34030
C/Genetics:
A/Gene: GDB:IGH@; IGHDIY1
A/Cross-references: GDB:I18731; OMIM:146910
A/Map position: 14q32.33-14q32.33
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 66.5%; Score 415.5; DB 2; Length 122;
Best Local Similarity 70.9%; Pred. No.1.4e-29;
Matches 83; Conservative 12; Mismatches 17; Indels 5; Gaps 4;

Qy 1 EVQLVESGGGLVQPGRSRLSCAVSGYSITSGYSWMNIRQAPGKGLEWVASITYDGSNTN- 59
:|||||:|||||:|||||:|:::|:|||||:|||||:|::|
Db 1 QVQLVESGGGVVPGRSRLSLCSAASGFTFS-YAMHWVRQAPGKLEWVAIVSYDGSKNY 59
:|||||:|||||:|||||:|:::|:|||||:|||||:|::|

Qy 60 YNPVKRITISRDTSKNTFYLMNSLRADTAVYYCARSHYFGHWHFA--VWVGQ 114
| |||||:|||||:|||||:|:::|:|||||:|||||:|::|
Db 60 YADSVKGRFTISRDNKNTLYLQWNSLRADTAVYYCARDRH--SSSWYGMVDVWGQG 115

RESULT 6
S48797
Ig heavy chain V region (anti-Sm, VH3/Dxp4/JH6) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 13-Jan-1995 #sequence_revision 13-Sep-1998 #text_change 23-Jul-1999
C/Accession: S48797; S26893
R/Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
submitted to the EMBL Data library, October 1994.
A/Description: Molecular characterization of natural human anti-Sm autoantibodies.
A/Reference number: S48797
A/Accession: S48797
A/Molecule type: mRNA
A/Residues: 1-128 <MAH>
A/Cross-references: EMBL:Z46379; NID:g587147; PIDN:CAA86512.1; PID:g1340168
R/Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A/Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V A/Reference number: S26895; MUID:93021117; PMID:1404388
A/Accession: S26893
A/Molecule type: DNA
A/Residues: 1-98 <TML>
A/Cross-references: EMBL:Z12350; NID:g32922; PIDN:CAA78220.1; PID:g32923
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 66.5%; Score 415.5; DB 2; Length 128;
Best Local Similarity 68.0%; Pred. No.1.5e-29;
Matches 83; Conservative 15; Mismatches 15; Indels 9; Gaps 4;

Qy 1 EVQLVESGGGLVQPGRSRLSCAVSGYSITSGYSWMNIRQAPGKGLEWVASITYDGSNTN- 59
:|||||:|||||:|||||:|:::~|:|||||:|||||:|::|
Db 1 QVQLVESGGGVVPGRSRLSLCSAASGFTFS-YGMHWVRQAPGKLEWVAIVTDGSKNY 59

```
Qy 60 YNPVKGRITISRDSKNTFYLMNSLRADTAATVYTCARGSHYF---CHWHF-----AVWG 112
Db 60 YADSVKGRFTISRDNKNTLYLMNSLRADTAATVYTCARDNYYYDSSGYYYYGMDVWG 119

Qy 113 QG 114
Db 120 QG 121

RESULT 7
Ig heavy chain - human
C:Species: Homo sapiens (man)
C>Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C:Accession: S31113
R:Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
Eur. J. Immunol. 22, 247-251, 1992
A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple
A:Reference number: S31104; MUID:92111633; PMID:1730252
A:Accession: S31113
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-121 <RAA>
A:Cross-references: EMBL:X62962
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 66.2%; Score 414; DB 2; Length 121;
Best Local Similarity 70.4%; Pred. No. 1.9e-29;
Matches 81; Conservative 14; Mismatches 18; Indels 2; Gaps 2;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNNWIRQAPGKLEWVASIT-YDGSN 59
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFS-YAMSVWRVQAPGKLEWVASISGSGSTY 59

Qy 60 YNPVKGRITISRDSKNTFYLMNSLRADTAATVYTCARGSHYFCHWHFPAVWGQ 114
Db 60 YADSVKGRFTISRDNKNTLYLMNSLRADTAATVYTCARDNYYYDSSGYYYYGMDVWGQ 114

RESULT 8
Ig heavy chain - human
C:Species: Homo sapiens (man)
C>Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C:Accession: S31117
R:Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
Eur. J. Immunol. 22, 247-251, 1992
A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple
A:Reference number: S31104; MUID:92111633; PMID:1730252
A:Accession: S31117
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-122 <RAA>
A:Cross-references: EMBL:X62967
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 65.7%; Score 410.5; DB 2; Length 122;
Best Local Similarity 71.6%; Pred. No. 4e-29;
Matches 83; Conservative 9; Mismatches 21; Indels 3; Gaps 3;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNNWIRQAPGKLEWVASITYDGSN- 59
Db 1 QVQLVESGGGVQPGGSLRLSCAASGFTFS-YGMEWVRVQAPGKLEWVASIVTDGSKNY 59

Qy 60 YNPVKGRITISRDSKNTFYLMNSLRADTAATVYTCARGSHYFCHWHF-HFAVWGQ 114
Db 60 YADSVKGRFTISRDNKNTLYLMNSLRADTAATVYTCARDNYYYDSSGYYYYGMDVWGQ 115
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RESULT 9

```
S31669
Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31669
R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnel, C.
submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
A:Reference number: S31585
A:Accession: S31669
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-141 <CDI>
A:Cross-references: EMBL:Z14212; NID:930959; PIDN:CAA78581.1; PID:930960
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>
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Query Match 65.7%; Score 410.5; DB 2; Length 141;
Best Local Similarity 70.7%; Pred. No. 4.6e-29;
Matches 82; Conservative 13; Mismatches 18; Indels 3; Gaps 3;
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Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNNWIRQAPGKLEWVASITYDGS-TN 59
Db 20 EVQLVESGGGLVQPGGSLRLSCAASGFTFS-YSNMVRVQAPGKLEWVSSISSSSYIY 78

Qy 60 YNPVKGRITISRDSKNTFYLMNSLRADTAATVYTCARGSHYFCH-WHFAVWGQ 114
Db 79 YADSVKGRFTISRDNKNTLYLMNSLRADTAATVYTCARGHLTGKGYFDLWGRG 134
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RESULT 10

```
I37780
Ig variable region (VDJ) (clone T20-11) - human (fragment)
```

```
C:Species: Homo sapiens (man)
C>Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 23-Jul-1999
C:Accession: I37780; S25474
R:Demaision, C.; Chastagner, P.; Theze, J.; Zouali, M.
Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994
A:Title: Somatic diversification in the heavy chain variable region genes expressed by h
A:Reference number: A36876; MUID:94119917; PMID:8290556
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A:Accession: I37780
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-147 <RES>
A:Cross-references: EMBL:X67943; NID:933578; PIDN:CAA48130.1; PID:933579
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:28-111/Domain: immunoglobulin homology <IMM>
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Query Match 65.7%; Score 410.5; DB 2; Length 147;
Best Local Similarity 70.3%; Pred. No. 4.8e-29;
Matches 83; Conservative 12; Mismatches 18; Indels 5; Gaps 3;
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Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNNWIRQAPGKLEWVASITYDGSN- 59
Db 14 EVQLVESGGGLVQPGGSLRLSCAASGFTFS-YMWSVVRVQAPGKLEWVANIKDQSEKY 72

Qy 60 YNPVKGRITISRDSKNTFYLMNSLRADTAATVYTCARGSHYFCHWHF---AVWGQ 114
Db 73 YADSVKGRFTISRDNKNTLYLMNSLRADTAATVYTCARDGEGWGLYYGYGMDVWGQ 130
```

RESULT 11

```
S19666
```

```
Ig heavy chain V region (VH3DJH4) - human
C:Species: Homo sapiens (man)
```

```
C>Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
C:Accession: S19666
R:Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter,
J. Mol. Biol. 222, 581-597, 1991
```

A;Accession: S31107
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-119 <RAA>
A;Cross-references: EMBL:X62955
A;Note: The nucleotide sequence was submitted to the EMBL Data Library, October 1980.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 65.3%; Score 408; DB 2; Length 119;
Best Local Similarity 70.9%; Pred. NO. 6.4e-29;
Matches 83; Conservative 13; Mismatches 13; Indels 8; Gaps 4;

Search completed: June 3, 2005, 09:17:51
Job time : 8.09576 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 3, 2005, 08:31:37 ; Search time 32.7497 Seconds

(without alignments)
1782.523 Million cell updates/sec

Title: US-10-791-619-12

Perfect score: 625

Sequence: 1 EVQLVSGGGLVQPGSRL.....YCARSHYFGHHFAVWQG 114

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	412	65.9	470	Q6PJA4	Q6pia4 homo sapien
2	410	65.6	113	Q9UL90	Q9ul90 homo sapien
3	403.5	64.6	118	Q9UL72	Q9ul72 homo sapien
4	400.5	64.1	613	Q8WUK1	Q8wuk1 homo sapien
5	400	64.0	121	Q9UL71	Q9ul71 homo sapien
6	400	64.0	240	Q65ZC9	Q65zc9 homo sapien
7	400	64.0	466	Q6IN78	Q6in78 homo sapien
8	398.5	63.8	606	Q6GMY2	Q6gmy2 homo sapien
9	397	63.5	478	Q6PI81	Q6pi81 homo sapien
10	395	63.2	116	Q9UL93	Q9ul93 homo sapien
11	395	63.2	472	Q6N089	Q6n089 homo sapien
12	394.5	63.1	473	Q6MZV7	Q6mzv7 homo sapien
13	393.5	63.0	118	Q9UL91	Q9ul91 homo sapien
14	392.5	62.8	122	1 HV3G HUMAN	P01768 homo sapien
15	392.5	62.8	147	Q9Y509	Q9y509 homo sapien
16	392	62.7	493	Q6GMX2	Q6gmx2 homo sapien
17	392	62.7	597	Q96BB9	Q96bb9 homo sapien
18	391	62.6	120	1 HV3E HUMAN	P01766 homo sapien
19	391	62.6	464	Q6MZU6	Q6mzu6 homo sapien
20	390	62.4	123	1 HV24 MOUSE	P01793 mus musculus
21	387.5	62.0	116	1 HV05 CARAU	P19181 carassius a
22	387.5	62.0	475	Q6MZQ6	Q6mzq6 homo sapien
23	387.5	62.0	573	Q8WU38	Q8wu38 homo sapien
24	384	61.4	493	Q8NCL6	Q8ncl6 homo sapien
25	384	61.4	499	Q8NSK4	Q8nsk4 homo sapien
26	383.5	61.4	112	2 Q9HCC1	Q9hcc1 homo sapien
27	383	61.3	117	1 HV3C HUMAN	P01764 homo sapien
28	379	60.6	479	2 Q9M22	Q9m22 mus musculus
29	378.5	60.6	494	2 Q96K68	Q96k68 homo sapien
30	375	60.0	115	1 HV3F HUMAN	P01767 homo sapien
31	375	60.0	121	1 HV3JF HUMAN	P01771 homo sapien

32	375	60.0	123	1 HV22 MOUSE	P01791 mus musculus
33	374.5	59.9	119	1 HV37 MOUSE	P01807 mus musculus
34	373.5	59.8	487	2 Q5ZVX0	Q6zvx0 homo sapien
35	372	59.5	119	1 HV31 HUMAN	P01770 homo sapien
36	371.5	59.4	487	2 Q99KA4	Q99ka4 mus musculus
37	371	59.4	487	2 Q80Z17	Q80zi7 mus musculus
38	370	59.2	123	1 HV23 MOUSE	P01792 mus musculus
39	370	59.2	137	1 HV46 MOUSE	P01822 mus musculus
40	369.5	59.1	136	2 Q6LBQ5	Q6lbq5 mus musculus
41	368.5	59.0	544	2 Q6PJ95	Q6pj95 homo sapien
42	367.5	58.8	122	1 HV21 MOUSE	P01790 mus musculus
43	367.5	58.8	465	2 Q6P6C4	Q6p6c4 homo sapien
44	367.5	58.8	479	2 Q6MZV6	Q6mzv6 homo sapien
45	367	58.7	119	2 Q920E7	Q920e7 mus musculus

ALIGNMENTS

RESULT 1

Q6PJA4 PRELIMINARY; PRT; 470 AA.

AC Q6PJA4;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Stapleton M., Wozniak D., Sodergren E.J., Lu X., Gibbs R.A., Raba S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Small D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX Strausberg R.;
RA Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018747; AAH18747.1; --
DR HSSP; P01861; 1ADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.

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KW Hypothetical protein.
SQ SEQUENCE 470 AA; 51715 MW; 7B49556A11PFD99 CRC64;

Query Match 65.6%; Score 410; DB 2; Length 470;
Best Local Similarity 72.4%; Pred. No. 9.5e-33;
Matches 82; Conservative 11; Mismatches 17; Indels 4; Gaps 4;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSNWIRQAPGKGLWEVASITVDGSGTNY 60
Db 20 EVQLVESGGGLVQPGGSLRLSCVVGSTFSS-YWMSWVRQAPGKGLWEVANIKDGSSEKY 78

Qy 61 N-PSVKGRITISRDNSKNTFLQNSLRADETAVYYCAR-GSHYFGHHFAVWGQG 114
Db 79 YVDSVKGRFTISRDNKSNLYLQNSLRADETAVYYCARDGGSWYRDW-FDPWGQG 133

RESULT 2
Q9UL90 PRELIMINARY; PRT; 113 AA.
AC Q9UL90;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN 1
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035042; AAD56278.1; -.
DR PIR; S21205; S21205.
DR HSP; P01783; IIGC.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 118
SQ SEQUENCE 118 AA; 12872 MW; B4D1A5944B2D5CCA CRC64;

Query Match 64.6%; Score 403.5; DB 2; Length 118;
Best Local Similarity 73.0%; Pred. No. 1.5e-32;
Matches 84; Conservative 9; Mismatches 17; Indels 5; Gaps 4;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSNWIRQAPGKGLWEVASITYD-GSTN 59
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTVSSNY-MNWVRQAPGKGLSEV-SVTYGGSSY 58

Qy 60 YNPSVKGRITISRDNSKNTFLQNSLRADETAVYYCARGSHYFGHHFAVWGQG 114
Db 59 YADSVKGRFTISRDNKSNLYLQNSLRADETAVYYCARDR--FGEFLFDYWGQG 111

RESULT 4
Q8WUK1 PRELIMINARY; PRT; 613 AA.
AC Q8WUK1;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN 1
RP SEQUENCE FROM N.A.
RX TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.J., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Besak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN 2
RP SEQUENCE FROM N.A.
RX TISSUE=Primary B-Cells;
RA Strausberg R.;
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KW Hypothetical protein.
SQ SEQUENCE 470 AA; 51715 MW; 7B49556A11PFD99 CRC64;

Query Match 65.6%; Score 410; DB 2; Length 470;
Best Local Similarity 72.4%; Pred. No. 9.5e-33;
Matches 82; Conservative 11; Mismatches 17; Indels 4; Gaps 4;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSNWIRQAPGKGLWEVASITVDGSGTNY 60
Db 20 EVQLVESGGGLVQPGGSLRLSCVVGSTFSS-YWMSWVRQAPGKGLWEVANIKDGSSEKY 78

Qy 61 N-PSVKGRITISRDNSKNTFLQNSLRADETAVYYCAR-GSHYFGHHFAVWGQG 114
Db 79 YVDSVKGRFTISRDNKSNLYLQNSLRADETAVYYCARDGGSWYRDW-FDPWGQG 133

RESULT 2
Q9UL90 PRELIMINARY; PRT; 113 AA.
AC Q9UL90;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN 1
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035024; AAD56260.1; -.
DR PIR; S78486; S78486.
DR HSP; P01772; 2P84.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 113
SQ SEQUENCE 113 AA; 12437 MW; E57FDD19086D07F CRC64;

Query Match 65.6%; Score 410; DB 2; Length 113;
Best Local Similarity 71.3%; Pred. No. 3.2e-33;
Matches 82; Conservative 9; Mismatches 14; Indels 10; Gaps 3;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSNWIRQAPGKGLWEVASITVDGSGT- 59
Db 1 EVQLVESGGGVQPGGSLRLSCAASGFTFSS-YGMHWVRQAPGKGLWEVAFIRYDGSNKY 59

Qy 60 YNPSVKGRITISRDNSKNTFLQNSLRADETAVYYCARGSHYFGHHFAVWGQG 114
Db 60 YADSVKGRFTISRDNKSNLYLQNSLRADETAVYYCAKDLNY-----WGQG 106

RESULT 3
Q9UL72 PRELIMINARY; PRT; 118 AA.
AC Q9UL72;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

RL EMBL: BC020240; AAH02040.1; --
DR PIR: F36005; F36005.
DR PIR: G36005; G36005.
DR PIR: PH1642; PH1642.
DR PIR: PH1643; PH1643.
DR PIR: PH1645; PH1645.
DR PIR: PH1646; PH1646.
DR PIR: PL0098; PL0098.
DR PIR: PL0120; PL0120.
DR PIR: S15590; S15590.
DR PIR: S31116; S31116.
DR PIR: S31119; S31119.
DR PIR: S70442; S70442.
DR HSP: P01861; 1ADQ.
DR Pfam: PF07654; Cl-set; 4.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS0835; IG LIKE; 5.
DR PROSITE: PS0290; IG MHC; UNKNOWN 3.
SQ SEQUENCE 613 AA; 67295 MW; 60C7F5950671E315 CRC64;

Query Match 64.1%; Score 400.5; DB 2; Length 613;
Best Local Similarity 67.5%; Pred. No. 1.8e-31;
Matches 81; Conservative 11; Mismatches 15; Indels 13; Gaps 4;
QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNWIRQAPGKLEWVASITYDGSTN- 59
Db 20 QVQLVESGGGLVQPGGSLRLSCAASGFTFSS-YGMHWVRQAPGKLEWVAVISYDGSNRY 78
QY 60 YNPYSVKGRITISRDTSKNTLYQMNSLRADTAVYYCARGSHYFGHWH-----FAVWGQ 114
Db 79 YADSVKGRFTISRDNKNTLYQMNSLRADTAVYYCAK-----DWSEGVETFDINGQ 132

RESULT 5
Q9UL71 PRELIMINARY; PRT; 121 AA.
AC Q9UL71
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035043; AAD56279.1; --
DR HSP: P01852; INFN.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003596; IG_v.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS0835; IG LIKE; 1.
FT NON TER 1 121
FT NON TER 121 121
SQ SEQUENCE 121 AA; 13154 MW; 2F045CFA5D50736 CRC64;

Query Match 64.0%; Score 400; DB 2; Length 121;
Best Local Similarity 68.7%; Pred. No. 3.4e-32;
Matches 79; Conservative 14; Mismatches 20; Indels 2; Gaps 2;
QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNWIRQAPGKLEWVASITYD-GSTN 59
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTF-DGYAMHWVRQAPGKLEWVLSISGGGSTY 59

Query Match 64.0%; Score 400; DB 2; Length 121;
Best Local Similarity 68.7%; Pred. No. 3.4e-32;
Matches 79; Conservative 14; Mismatches 20; Indels 2; Gaps 2;
QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNWIRQAPGKLEWVASITYD-GSTN 59
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTF-DGYAMHWVRQAPGKLEWVLSISGGGSTY 59

QY 60 YNPYSVKGRITISRDTSKNTLYQMNSLRADTAVYYCARGSHYFGHWHFAVWGQ 114
Db 60 YADSVKGRFTISRDNKNTLYQMNSLRADTAVYYCARGKVTIYDRFDINGQ 114

RESULT 6
Q65ZC9 PRELIMINARY; PRT; 240 AA.
AC Q65ZC9
DT 25-OCT-2004 (TRENBLrel. 28, Created)
DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE Single-chain Fv (Fragment).
GN Name=scFv;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C1q/7;
RX MEDLINE=97362799; PubMed=9219263;
RA Kontermann R.E., Wing M.G., Winter G.;
RT "Complement recruitment using bispecific diabodies."
RL Nat. Biotechnol. 15:629-631(1997).
DR EMBL: Y13056; CAA73499.1; --
DR InterPro: IPR003599; IG.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003596; IG_v.
DR Pfam: PF00047; IG; 2.
DR SMART: SM00409; IG; 2.
DR SMART: SM00406; IGV; 2.
DR PROSITE: PS0835; IG LIKE; 2.
FT NON TER 1 240
FT NON TER 240 240
SQ SEQUENCE 240 AA; 25569 MW; FDCFD3645F64B373 CRC64;

Query Match 64.0%; Score 400; DB 2; Length 240;
Best Local Similarity 69.2%; Pred. No. 7.2e-32;
Matches 81; Conservative 12; Mismatches 14; Indels 10; Gaps 4;
QY 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNWIRQAPGKLEWVASITYDGSTN- 59
Db 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFSS-YGMHWVRQAPGKLEWVAVISYDGSNRY 59
QY 60 YNPYSVKGRITISRDTSKNTLYQMNSLRADTAVYYCARGSHYFGHWHFAV--WQGG 114
Db 60 YADSVKGRFTISRDNKNTLYQMNSLRADTAVYYCAR-----DWGSDLPWGKG 110

RESULT 7
Q6IN78 PRELIMINARY; PRT; 466 AA.
AC Q6IN78
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE IG_H1 protein.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RX MEDLINE=2386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

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RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Jones S.J., Marra M.A.,
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC072419; AAH72419.1; -.
DR HSP; P01861; 1ADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG1; 3.
DR SMART; SM00407; IGL1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 466 AA; 50853 MW; 53EB0BCED81076E CRC64;

Query Match 64.0%; Score 400; DB 2; Length 466;
Best Local Similarity 69.3%; Pred. No. 1.5e-31;
Matches 79; Conservative 12; Mismatches 19; Indels 4; Gaps 2;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAVGSYITSGYSWNIROAPGKLEWVASITVDGSTNY 60
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
20 EVQLVESGGGLVQPGGSLRLSCAVGSYITSGYSWNIROAPGKLEWVASITVDGSTNY 78

Qy 61 NPSYKGRITISRDNSKNTLYQMNSLRADETAVYTCARGSHYFGHWFVWGQG 114
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
79 ADSVKGRFTISRDNSKNTLYQMNSLRADETAVYTCARGNYV---PAAPWGQG 129

RESULT 8
Q6GMV2 PRELIMINARY; PRT; 606 AA.
AC Q6GMV2
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

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RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC073758; AAH73758.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 4.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGL1; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 3.
KW Hypothetical protein.
SQ SEQUENCE 606 AA; 66184 MW; B6B38B5114E4C55 CRC64;

Query Match 63.8%; Score 398.5; DB 2; Length 606;
Best Local Similarity 63.3%; Pred. No. 2.8e-31;
Matches 81; Conservative 14; Mismatches 18; Indels 15; Gaps 3;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAVGSYITSGYSWNIROAPGKLEWVASITVDGS-TN 59
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
20 QVQLVESGGGLVQPGGSLRLSCAVGSYITSGYSWNIROAPGKLEWVASITVDGS-TN 78

Qy 60 YNPSTVGRITISRDNSKNTLYQMNSLRADETAVYTCARGSH-----YFGHW 106
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
79 YADSVKGRFTISRDNSKNTLYQMNSLRADETAVYTCARGNGIAAAGRVVYAEIDYIY 138

Qy 107 HFAVWGQG 114
Db |||||
139 GMDVWGQG 146

RESULT 9
Q6PI81 PRELIMINARY; PRT; 478 AA.
AC Q6PI81
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

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RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
RA Fahy J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC041037; AAHA1037.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; CI-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 478 AA; 52666 MW; 17BED38D917970D6 CRC64;

Query Match 63.5%; Score 397; DB 2; Length 478;
Best Local Similarity 65.3%; Pred. No. 3.1e-31;
Matches 81; Conservative 15; Mismatches 16; Indels 12; Gaps 4;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNNWIRQAPGKLEWVASITVDGSTN 60
Db 2 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNNWIRQAPGKLEWVASITVDGSTN 78
Qy 61 N-PSVKGRITISRDSKNTFYLQMSLRAEDTAVYYCAR-----GSHYFGHWHFAV 110
Db 79 YVDSYKGRFTISRDNKNSLYLQMSLRAEDTAVYYCARFESTTWTNADYY-YFYMDV 137
Qy 111 WGQG 114
Db 138 WGKG 141

RESULT 10
Q9UL93
ID Q9UL93 PRELIMINARY; PRT; 116 AA.
AC Q9UL93
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RG The German Human CDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640627; CAE45781.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; CI-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;

Query Match 63.2%; Score 395; DB 2; Length 472;
Best Local Similarity 66.7%; Pred. No. 4.8e-31;
Matches 78; Conservative 16; Mismatches 19; Indels 4; Gaps 3;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNNWIRQAPGKLEWVASITYD-GSTN 59
Db 20 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNNWIRQAPGKLEWVASISWNSG 78
Qy 60 YNPSVKGRITISRDSKNTFYLQMSLRAEDTAVYYCAR--GSHYFGHWHFAVWGQ 114
Db 79 YADSVKGRFTISRDNKNSLYLQMSLRAEDTALYYCAKEIGAHNFYYGYGMDVWGQ 135

RESULT 12
Q6MZV7
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DR HSSP; P01772; 2PB4.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
FT NON TER 1
FT NON TER 116
SQ SEQUENCE 116 AA; 12434 MW; 0DA0348154DD6061 CRC64;

Query Match 63.2%; Score 395; DB 2; Length 116;
Best Local Similarity 70.2%; Pred. No. 1e-31;
Matches 80; Conservative 10; Mismatches 18; Indels 6; Gaps 3;

Qy 2 VOLVESGGGLVQPGGSLRLSCAASGYSITSGYSNNWIRQAPGKLEWVASITYDGS 60
Db 1 VOLVESGGGVQPGSLRLSCAASGFTFSS-YAMHWVRQAPGKLEWVASIDGSNKYY 59
Qy 61 NPSVKGRITISRDSKNTFYLQMSLRAEDTAVYYCARGSHYFGHWHFAVWGQ 114
Db 60 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAMYYCAGS---GGGLGLGYWGQ 109

RESULT 11
Q6N089
ID Q6N089 PRELIMINARY; PRT; 472 AA.
AC Q6N089
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686P15220.
GN Name=DKFZp686P15220;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RG The German Human CDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640627; CAE45781.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; CI-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;

Query Match 63.2%; Score 395; DB 2; Length 472;
Best Local Similarity 66.7%; Pred. No. 4.8e-31;
Matches 78; Conservative 16; Mismatches 19; Indels 4; Gaps 3;

Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNNWIRQAPGKLEWVASITYD-GSTN 59
Db 20 EVQLVESGGGLVQPGGSLRLSCAASGFTF--DDYAMHWVRQAPGKLEWVSGISWNSG 78
Qy 60 YNPSVKGRITISRDSKNTFYLQMSLRAEDTAVYYCAR--GSHYFGHWHFAVWGQ 114
Db 79 YADSVKGRFTISRDNKNSLYLQMSLRAEDTALYYCAKEIGAHNFYYGYGMDVWGQ 135

RESULT 12
Q6MZV7
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ID QGMZV7 PRELIMINARY; PRT; 473 AA.
AC QGMZV7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686C11235.
GN Name=DKFZp686C11235;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUP=Human small intestine;
RG The German Human cDNA Consortium;
RA Bloecker H., Boecker M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640853; CAB45920.1; -;
DR HSP; P01861; IADQ.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG-MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 52121 MW; 9476EAE4C0BFC447 CRC64;

Query Match 63.1%; Score 394.5; DB 2; Length 473;
Best Local Similarity 64.4%; Pred. No. 5.4e-31;
Matches 76; Conservative 18; Mismatches 19; Indels 5; Gaps 3;
Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNMIRQAPGKLEWVASITVDGST-N 59
Db 20 EQIVESGGGLVQPGGSLRLSCAASGFTFS-FENMVRQAPGKLEWLSYITSGNIVY 78
Qy 60 YNPVSVKGRITISRDSDSKNTFYLNLSRAEDTAVYICARGSHYFGHWH---FAVWGQG 114
Db 79 YADSLQGRFTISRDNARNSLYLNLSRAEDTAVYICARQNEHTSPWYPSFDYWGQG 136

RESULT 13
Q9UL91
ID Q9UL91 PRELIMINARY; PRT; 118 AA.
AC Q9UL91;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
DR EMBL; AF035023; AAD56259.1; -;
DR PIR; PH0875; PH0875.
DR PIR; S21205; S21205.
DR PIR; S30531; S30531.
DR HSP; P01783; IIGC.

DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 1 118
SQ SEQUENCE 118 AA; 12843 MW; D0633949F2AC149D CRC64;
Query Match 63.0%; Score 393.5; DB 2; Length 118;
Best Local Similarity 69.5%; Pred. No. 1.5e-31;
Matches 82; Conservative 9; Mismatches 16; Indels 11; Gaps 4;
Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNMIRQAPGKLEWVASITVDGST-- 58
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFS-YSMNVVRQAPGKLEWV---SYISITII 56
Qy 59 --NPNVSVKGRITISRDSDSKNTFYLNLSRAEDTAVYICARGSHYFGHWHFAVWGQ 114
Db 57 TIYYADSVKGRFTISRDNARNSLYLNLSRAEDTAVYICARGD---SSEAFDIWGQ 111
RESULT 14
HV3G_HUMAN
ID HV3G_HUMAN STANDARD; PRT; 122 AA.
AC P01768;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig heavy chain V-III region CAM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=81013859; PubMed=6774332;
RA Lehman D.W., Putnam F.W.;
RT "Amino acid sequence of the variable region of a human mu chain: location of a possible JH segment.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243 (1980).
CC -I- MISCELLANEOUS: This mu chain was isolated from the plasma of a patient with macroglobulinemia.
CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02051; M3HUAM.
DR HSP; P01772; 2PB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region; Pyroliidone carboxylic acid.
FT DOMAIN 1 112 IG-like.
FT MOD_RES 1 1 Pyroliidone carboxylic acid.
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 13668 MW; A42D0F17D252F1C2 CRC64;
Query Match 62.8%; Score 392.5; DB 1; Length 122;
Best Local Similarity 64.7%; Pred. No. 1.9e-31;
Matches 75; Conservative 16; Mismatches 22; Indels 3; Gaps 3;
Qy 1 EVQLVESGGGLVQPGGSLRLSCAASGYSITSGYSNMIRQAPGKLEWVASITVDGSTNY 60
Db 1 QVELVESGGGVZPGRSLRLSCAASGFTF-SNYAMHWVRQPPGKLEWVAIVYBGBBK 59
Qy 61 NP-SVKGRITISRDSDSKNTFYLNLSRAEDTAVYICARGSHYFGHWH-PAVWGQ 114
Db 60 YASVKGKRTISRDSKNTLYLNLSRAEDTAVYICARDRPLYGBTRAFNYWGQ 115


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RESULT 15
Q9Y509
ID Q9Y509 PRELIMINARY; PRT; 147 AA.
AC Q9Y509;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Vh3 protein (Fragment).
GN Name=Vh3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96071149; PubMed=7475288;
RA Cao J., Vescio R.A., Rettig M.B., Hong C.H., Kim A., Lee J.C.,
RA Lichtenstein A.K., Berenson J.R.;
RT "A CD10-positive subset of malignant cells is identified in multiple
RT myeloma using PCR with patient-specific immunoglobulin gene primers.";
RL Leukemia 9:1348-1353(1995).
DR EMBL; S80860; AAD14339.1; -.
DR HSSP; P01842; 1AOK.
DR GO; GO:0005887; C:integral to plasma membrane; NAS.
DR GO; GO:0016066; P:cellular defense response (sensu Vertebrata); NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
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Query Match 62.8%; Score 392.5; DB 2; Length 147;
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Db 1 QVHLVESGGGVVQPGKSLRLSCEASGFTF-STYGMVWVRQAPGKGLDWVALISYDGSQY 59

Qy 61 NP-SVKGRITISRDSDKNTFYLMNSLRAEDTAVYVCARGSHYF---GHWHFAV--WGQG 114
Db 60 YAGSVKGRFTISRDNSKNTLYLQMTSLRVEDTAVYVCADKGNYPDSVGYGIDYWGQG 119

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